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Hepatitis
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Synthetic
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                                                           (without alignments)
444.918 Million cell updates/sec
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                                                                                                      .... CSFSIFLLALLSCLTTPASA 191
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Aar96546 H
Aar22137 H
Aar38278 N
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Adj10436 B
Adj10438 B
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Aar92976
                                                  October 30, 2004, 01:28:51 ; Search time 154 Seconds
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5.1.6
Compugen Ltd.
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                                                                                                                                                  2002273 segs, 358729299 residues
version 5
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Maximum Match 100%
Listing first 45 summaries
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AAR74047
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AAR38278
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ADJ10438
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1045
1 MSTLPKPQRKTKRNTNRRPT.
GenCore (c) 1993
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  geneseqp1980s:*
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geneseqp2003bs:*
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Match Length
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Abp71460 Amino aci	ABP71460	9	3011	93.4	916	45
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	AAU79221	Ŋ	3011	93.4	916	43
	AAU84597	Ŋ	3011	93.4	916	42
	AAB31169	4	3011	93.4	976	41
	AAB59173	4	3011	93.4	976	40
	AAW98020	N	3011	93.4	916	39
_	AAW77398	~1	3011	93.4	976	38
	AAW77397	N	3011	93.4	976	37
	AAR79232	~	3011	93.4	916	36
	AAR40120	0	3011	93.4	916	35
	AAR40119	~	3011	93.4	976	34
	ADM24822	7	3002	93.4	976	33
	AAE00442	4	2984	93.4	916	32
	AAE00447	4	2984	93.4	976	31
	AAE00449	4	2984	93.4	916	30
	AAR79221	~	1648	93.4	916	29
_	AAW12715	7	1006	93.4	916	28
	AAR79222	7	967	93.4	916	27
_	AAR67591	N	502	93.4	926	56

ALIGNMENTS

AAR92936-R92987 are HCV core proteins derived from 52 different HCV isolates. Isolated cDNA sequences are used for the prodn. of primers useful for detecting the presence of HCV in a sample, the primers are also useful for HCV genotyping. Proteins encoded by the CDNAs can be used in vaccines for immunising against HCV infection. The proteins may also be used to detect antibodies against HCV in serum, saliva, lymphocytes or other mononuclear cells. The antibodies may be used in the prevention of DNA and amino acid sequence of HCV envelope 1 and core proteins - used to determine HCV genotype and as vaccines against HCV infection. HCV; E1; envelope 1; core protein; HCV genotyping; antibody; vaccine; hepatitis. Hepatitis C virus isolate HK2 core protein. AAR92987 standard; protein; 191 AA. Claim 4; Page 223; 340pp; English Purcell RH; 95WO-US010398. 94US-00290665. (USSH) US SEC DEPT HEALTH entry) (first Bukh J, Miller RH, WPI; 1996-139709/14 Hepatitis C virus. Sequence 191 AA; N-PSDB; AAT16661 HCV infection WO9605315-A2 15-AUG-1995; 15-AUG-1994; 02-0CT-1996 22-FEB-1996 AAR92987;

Query Match 100.0%; Score 1045; DB 2; Length 191; Best Local Similarity 100.0%; Pred. No. 2.5e-90;

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hepatitis.
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                           RROPIPKARQPOGRHWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPHWGPNDPRRRSRNLG
                                                                                             KVIDTLTCGFADLMGYIPVVGAPLGGVAAALAHGVRAIEDGINYATGNLPGCSFSIFLLA
                                                                                                            KVIDTLTCGFADLMGYIPVVGAPLGGGVAAALAHGVRAIEDGINYATGNLPGCSFSIFLLA
                  MSTLPKPQRKTKRNTNRRPTDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRG
                                                                                                                                                                                                                                                                          envelope 1; core protein; HCV genotyping; antibody; vaccine;
Gaps
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Mismatches
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Conservative
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Best Local Simil
Matches 181; (
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Matches
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Conservative

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RROPIPKAROPEGRSWAOPGYPWPLYGNEGCGWAGWLLSPRGSRPSWGPNDPRRRSRNLG
                                              KV1DTLTCGFADLMGY1PVVGAPLGGVAAALAHGVRA1EDG1NYATGNLPGCSFS1FLLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HCV; E1; envelope 1; core protein; HCV genotyping; antibody; vaccine;
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determine HCV genotype and as vaccines against HCV infection
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93.7%;
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Best Local Similarity 93.7
Matches 179; Conservative
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                                                                                                                                                                                                                                                                                                                               envelope 1; core protein; HCV genotyping; antibody; vaccine;
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Pred. No. 2.1e-84;
                                                                                                                                                                                                                                                                                      Hepatitis C virus isolate 28 core protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 4; Page 211-212; 340pp; English.
                                                                                                                                                                       AAR92973 standard; protein; 191 AA
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                                                          Miller RH,
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                       Hepatitis C virus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HCV infection
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-AUG-1995;
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Matches 179;
                                                                                                                                                                                                                                                                                                                                               hepatitis.
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AAR92936-R92987 are HCV core proteins derived from 52 different HCV isolates. Isolated cDNA sequences are used for the prodn. of primers useful for detecting the presence of HCV in a sample, the primers are also useful for HCV genotyping. Proteins encoded by the cDNAs can be used in vaccines for immunising against HCV inserion. The proteins may also be used to detect antibodies against HCV in serum, saliva, lymphocytes or other mononuclear cells. The antibodies may be used in the prevention of
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                                                                                                                                                                                                   envelope 1; core protein; HCV genotyping; antibody; vaccine;
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Pred. No. 2.6e-84;
5; Mismatches 7; Indels
                                                                                                                                                 Hepatitis C virus isolate HK3 core protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 4; Page 194-195; 340pp; English.
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AAR92953 standard; protein; 191 AA
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93.7%;
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N-PSDB; AAT16627.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                           Hepatitis C virus.
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                                                                                                                                                                                              HCV; E1; el hepatitis.
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N-PSDB; AAT16650
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                                                                                                                   (USSH ) US SEC
                                                                                                                                                                                                                                                                                                             HCV infection
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hepatitis.
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                                                                                                                                       Bukh J,
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                                                envelope 1; core protein; HCV genotyping; antibody; vaccine;
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                                                                                                                                                                                                                                                                                                                                                                                                            Score 980; DB 2; I Pred. No. 3.3e-84; 4; Mismatches 8;
                            Hepatitis C virus isolate DK13 core protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hepatitis C virus isolate Z6 core protein.
                                                                                                                                                                                                                                                                              Claim 4; Page 215-216; 340pp; English
                                                                                                                                                                                                  RH;
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Best Local Similarity 93.7
Matches 179; Conservative
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                                                                                                                                                                                                                   WPI; 1996-139709/14.
N-PSDB; AAT16652.
                                                                            Hepatitis C virus.
                                                                                                                                                                                                                                                                                                                                                                                         Sequence 191 AA;
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                                                                                                 WO9605315-A2
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        02-OCT-1996
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                                                E1;
                                                                                                                                                                                                 Bukh J,
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AAR92936-R92987 are HCV core proteins derived from 52 different HCV isolates. Isolated CDNA sequences are used for the prodn. of primers useful for detecting the presence of HCV in a sample, the primers are also useful for HCV genotyping. Proteins encoded by the CDNAs can be used in vaccines for immunishing against HCV in fection. The proteins may also be used to detect antibodies against HCV in serum, saliva, lymphocytes or other mononuclear calls. The antibodies may be used in the prevention of
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Pred. No. 5.1e-84;
5; Mismatches 8;
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                                                                                                                                                                                                                                                                                                                                                                       Purcell RH;
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93.2%;
                                                                                                                                                                                                                                                                                                          DEPT HEALTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 93.2
Matches 178; Conservative
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                                                                                                                                                                                                                                                                                                                                                                       Miller RH,
                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1996-139709/14
Hepatitis C virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hepatitis C virus.
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DNA and amino acid sequence of HCV envelope 1 and core proteins - used to determine HCV genotype and as vaccines against HCV infection.

Claim 4; Page 214-215; 340pp; English

AAR92936-R92987 are HCV core proteins derived from 52 different HCV isolates. Isolated cDNA sequences are used for the prodn. of primers useful for detecting the presence of HCV in a sample, the primers are also useful for HCV genotyping. Proteins encoded by the cDNAs can be used in vaccines for immunising against HCV infection. The proteins may also be used to detect antibodies against HCV in serum, saliva, lymphocytes or other mononuclear cells. The antibodies may be used in the prevention of

Sequence 191 AA;

ö RRQPIPKARQPQGRHWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPHWGPNDPRRRSRNLG 120 120 KVIDTLTCGFADLMGYIPVVGAPLGGVAAALAHGVRAIEDGINYATGNLPGCSFSIFLLA 180 9 1 MSTLPKPORKTKRNTNRRPTDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRG Gaps . 0 93.5%; Score 977; DB 2; Length 191; 93.2%; Pred. No. 6.3e-84; 8; Indels 5; Mismatches Matches 178; Conservative LLSCLTTPASA 191 LLSCLTVPASA 191 Best Local Similarity 61 61 121 121 181 Query Match 181 ò 셤 à g à qq ò d

AAR74048 standard; protein; 196 AA. AAR74048; RESULT 9

nucleocapsid (revised)
(first entry) Synthetic HCV 25-MAR-2003 26-NOV-1995

protein.

Hepatitis C virus; vector; expression; prokaryotic cells; detection; diagnosis.

WO9511980-A2 Synthetic

04-MAY-1995.

94WO-US012166 25-OCT-1994;

93US-00141917 25-OCT-1993;

(USSH) US DEPT HEALTH & HUMAN SERVICES

Khudyakov Y, Fields HA;

1995-178872/23

N-PSDB; AAQ92071

Vector for expression of a synthetically produced protein coding DNA - pref. encodes the hepatitis C virus nucleo-capsid protein which can be used in the detection of HCV antibodies.

Disclosure; Page 37; 44pp; English.

The sequence is that of a synthetic nucleotide sequence encoding the hepatitis C virus nucleocapsid protein. The gene is positioned in a vector for efficient expression in prokaryotic calls. The expressed protein can be used in tests for the detection of antibodies specific for the HCV C protein. See also AAR74047. (Updated on 25-MAR-2003 to correct field.)

Sequence 196 AA;

Gaps ; Length 196; Indels 93.5%; Score 977; DB 2; Le 92.1%; Pred. No. 6.5e-84; Micmatches 9; Best Local Similarity 92.1 Matches 176; Conservative Local Similarity Query Match

0

180 121 KVIDTLTCGFADLMGYIPVVGAPLGGVAAALAHGVRAIEDGINYATGNLPGCSFSIFLLA 180 ð

g

181 LLSCLTTPASA 191 셤 à

181 LLSCLTVPASA 191

RESULT 10

AAR74047 standard; protein; 196 AA. AAR74047; AAR74047

Synthetic HCV nucleocapsid protein. 25-MAR-2003 26-NOV-1995

(revised)
(first entry)

Hepatitis C virus; vector; expression; prokaryotic cells; detection; diagnosis.

Synthetic.

WO9511980-A2

04-MAY-1995.

94WO-US012166. 25-OCT-1994;

93US-00141917 25-OCT-1993;

DEPT HEALTH & HUMAN SERVICES Sn (HSSn)

Khudyakov Y,

WPI; 1995-178872/23

Local

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the partities C virus subtypes different from subtypes 1a-c, 2a-d, 3a-f, 4a-c, 4, 5a and 6a. They esp. from the novel subtypes 1a-c, 2a-d, 3a-f, 3a-f, 4a-d, 7a-cor types 9,10 or 11. The sequences corresp. to the 5' untranslated region (WR), the Core/E1, NG or NS5B regions of the genome. This sequence represents amino acids 1-317 from the HCV types 9a and 7a isolates RR1. The new HCV types were isolated from patients with chronic HCV from the Benelux countries, France, Cameroon and Vietnam, because of their aberrant reactivities. The RNA was extracted, cDNA synthesised and PCR amplified, cloned and genotyped. The 5'UR, Core/E1 and NSSB regions over sequenced either directly or partially and used to classify the new viruses into (sub) types based on comparison with known sequences. The sequences were used to generate the peptides ARPS642+R86524. The sequences can also be used to synthesise probes and primers for the detection of HCV in a sample. The polypeptides can be used to detect anticed the network of the them the bodypeptides can be used to detect anticed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hepatitis C virus; non-A non-B virus; HCV-Hc59; antigen; vaccine; assay;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 RRQPIPKARQPQGRHWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPHWGPNDPRRRSRNLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MSTLPKPQRKTKRNTNRRPTDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MSTLPKPQRKTKRNTNRRPMDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KVIDTLTCGFADLMGYIPVVGAPLGGVAAALAHGVRAIEDGINYATGNLPGCSFSIFLLA
                                                                                                                                                                                                                                                                                                 The sequences AAR96526-R96578 represent novel sequences isolated from
                                                                                                                                                                        Hepatitis C virus poly:nucleic acid unique to unidentified sub:type used to develop probes and primers for new sub:types and vaccines to prevent and treat infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            93.5%; Score 977; DB 2; Length 31 93.7%; Pred. No. 1.1e-83; ive 3; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HCV-Hc59 capsid and envelope proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAR22137 standard; protein; 326 AA
                                                                                                                                                                                                                                                                 Claim 25; Fig 3; 150pp; English.
95EP-00870076.
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Best Local Similarity 93.77
Matches 179; Conservative
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                                      (INNO-) INNOGENETICS NV.
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non-B hepatitis virus.
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                                                                              Stuyver
                                                                                                                     WPI; 1996-251460/25.
N-PSDB; AAT27957.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 319 AA;
28-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27-AUG-2003
25-MAR-2003
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                                                                              Maertens G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 detection
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                                        Vector for expression of a synthetically produced protein coding DNA - pref. encodes the hepatitis C virus nucleo-capsid protein which can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RRQPI PKVRRPEGRTWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPSWGPTDPRRSRNLG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MSTIPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hepatitis C virus, subtype, polymerase chain reaction, amplification, PCR, primer, probe, antibody, infection.
                                                                                                                                                             sequence is that of a synthetic nucleotide sequence encoding the
                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hepatitis C virus types 9a(7a) isolates FR1 amino acids 1-317,
                                                                                                                                                                                                                                                                                                                                                  Length 196;
                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                          9
                                                                                                                                                                                                                                                                                                                                                  Score 977; DB 2;
Pred. No. 6.5e-84;
                                                                                                                                                                                                                                                                                                                                                                                        6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 label= Phe, Ser, Tyr, Cys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /label= Ser, Pro, Thr, Ala
                                                                                   used in the detection of HCV antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                         Disclosure; Page 35; 44pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAR96546 standard; peptide; 319 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'label= Ile, Met
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                94EP-00870166.
                                                                                                                                                                                                                                                                                                                                                  93.5%;
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                                                                                                                                                                                                                                                                                                                                                                     Similarity
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    N-PSDB; AAQ92070
                                                                                                                                                                                                                                                                                                            Sequence 196 AA;
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                                                                                                                                                                                                                                                                                                                                                                                    Matches 176;
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                                                                                                                                                                                                                                                                     field.)
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RESULT 11 AAR96546

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Gaps

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Length 319;

9 9 120 120

us-09-084-691b-206.rag

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180

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121 KVIDTLTCGFADLMGYIPVVGAPLGGVAAALAHGVRAIEDGINYATGNLPGCSFSIFLLA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The sequence is that of NANB hepatitis virus HC-OM gene polypeptide P-733 L. It may may be used in a system for detecting NANB hepatitis. This method is highly specific and sensitive, and can detect NANB hepatitis virus which could not be detected by conventional methods
  61 RRQPIPKARRPEGRTWAQPGYPWPLYGNEGCGWGGWLLSPRGSRPSWGPTDPRRRSRNLG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RRQPIPKARQPQGRHWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPHWGPNDPRRRSRNLG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Antigen related to non-A and non-B hepatitis virus - comprises non-translation region comprising 340 - 341 mols. of nucleotides, non-translation region comprising 1885 - 2551 mols. of nucleotides including
                                          1 MSTIPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MSTLPKPQRKTKRNTNRRPTDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRG
                                                                                                                                                                                                                                                                            Non-A, non-B; virus; polymerase chain reaction; detection; sensitive; specific; HCV; NANBH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 733;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                    NANB hepatitis virus HC-OM gene polypeptide P-733-1.
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7-1 No. 2.8e-83; 9; 7
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6; Mismatches
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                                                                                                                                                                       AAR38278 standard; protein; 733 AA.
                                                                                                                                                                                                                                                                                                                                                                                                             91JP-00196175.
                                                                                                                                                                                                                                                                                                                                                                                                                                      90JP-00153401.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                93.5%;
92.1%;
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les 176; Conservative
                                                                              181 LLSCLTTPASA 191
                                                                                                     LLSCLTVPASA 191
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                                                                                                                                                                                                                                                                                                                   Non-A.
non-B hepatitis virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1993-199637/25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (NAKA/) NAKAMURA T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  region 1,149 and,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; AAQ43888.
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Deoxyribonucleic acid sequence encoding non-A, non-B hepatitis virus - obtd. Hutch CS9 subgroup encoding polypeptide(s), useful as vaccines, and immuno reactive ABS for diagnosis of virus.
                                                                                                                                                                     "or Asn according to Seg No 46 (AAR22154), see CC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RROPIPKAROPOGRHWAOPGYPWPLYGNEGCGWAGWLLSPRGSRPHWGPNDPRRRSRNLG 120
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Pred. No. 1.1e-83;
5; Mismatches 9; Indels
               1. .326
/label= NANBV_structural_proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Prince AM;
                                                                                                                                                                                                                                                              /label= pref._envelope_antigen
                                                               1 .74
/label= pref._capsid_antigen
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/label= pref._capsid_antigen
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!label= pref._capsid_antigen
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/label= pref._capsid_antigen
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                                                                                                                                                                                                                                                 /label= envelope_protein
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ocation/Qualifiers
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/label= capsid
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91US-00748564.
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N-PSDB; AAQ22838.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                       Misc-difference
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Gaps

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181 LLSCLTVPASA 191

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New synthetic peptides for detecting antibodies to hepatitis C virus -
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                                                               Hepatitis C virus; peptides; antibodies; ELISA.
     AAR24440 standard; protein; 2894 AA.
                                                  Composite HCV HC-J1/CDC/CHI protein.
                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                               Pollet D, Maertens G,
                                                                                                                                                                                                                                                                                                                                                                                                     90EP-00124241.
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//abel= 2
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37 .56
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49. .68
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//3. .92
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1712. .1731

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263. .2282
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/label= 15
2275. .2294
/label= 16
2287. .2306
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2299. .2318
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/label= 9
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label= 19
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/label= 1
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                                (revised)
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                               25-MAR-2003
02-DEC-1992
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                                                                             Synthetic.
                  AAR24440;
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AAR24440
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RNA viruses frequently exhibit a high rate of spontaneous mutation, thus a virus is considered to be the same of equiv. to HCV if it exhibits a global homology of more than 70 percent with the HCV HC-VICCHII composite sequence. The peptide fragments of this DNA sequence indicated in the features table can immunologically mimic proteins encoded by HCV. Additional amino acids or chemical gps. may be added to either end of the peptides for the purpose of creating a linker arm for attachment to a carrier. The peptides can be used for the detection of antibodies specific for HCV. They may be used for the detection of antibodies specific for HCV. They may be used in the form of kits, opt. with reagents such as staphylococcal protein A, streptococcal protein G, avidin or streptavidin. The peptides may also be used as immunogens for raising antibodies. (Updated on 25-MAR-2003 to correct PN field.)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic antigens for the detection of hepatitis C virus antibodies - comprise portions of the HCV peptide sequence, for use in screening blood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 RRQPIPKARQPQGRHWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPHWGPNDPRRRSRNLG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MSTIPKPORKTKRNTNRRPODVKFPGGGOIVGGVYLLPRRGPRLGVRATRKTSERSQPRG
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useful in e.g. ELISA assays, and for detection of HCV antigens or as
                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Composite hepatitis C virus; HC-J1/CDC/CH1; HCV; non-A non-B; synthetic antigens; blood screening.
                                                                                                                                                                                                                                                                                                                                                     Length 2894;
                                                                                                                                                                                                                                                                                                                                                         Score 977; DB 2; Length 28
Pred. No. 1.3e-82;
6; Mismatches 9; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Composite hepatitis C virus (HC-J1/CDC/CHI).
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                                                       Disclosure, Fig 1; 32pp; English
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Best Local Similarity 92.1
Matches 176; Conservative
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181 LLSCLTVPASA 191
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hepatitis C virus
                                                                                                                                                                                                                                                                                                                         Sequence 2894 AA;
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07-NOV-1995
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                       immunogens
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us-09-084-691b-206.rag

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AAR70230 is the composite hepatitis C virus (HC-01/CDC/CHI) protein from which the synthetic HCV antigens described in AAR70210-R70229 were derived. These synthetic antigens can be used to screen blood, or blood products for the presence HCV, they can also be used in various specific assays for the detection of HCV antibodies, and antigens, or as immunogens. (Updated on 25-MAR-2003 to correct PN field.) (Updated on 25-MAR-2003 to correct PN field.)
                                       Disclosure, Fig 1; 51pp; English.
and blood products.
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Gaps 0; Score 977; DB 2; Length 2894; Pred. No. 1.3e-82; 6; Mismatches 9; Indels (Query Match 93.5%; Best Local Similarity 92.1%; Matches 176; Conservative (Sequence 2894 AA;

61 RRQPIPKVRRPEGRTWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPSWGPTDPRRRSRNLG 120 RROPI PKAROPOGRHWAOPGYPWPLYGNEGCGWAGWLLSPRGSRPHWGPNDPRRRSRNLG 120 19

à qq $\stackrel{\triangleright}{\sigma}$ qq à g ð d

Search completed: October 30, 2004, 01:42:44 Job time : 157 secs

[[[[]]]] LLSCLTVPASA 191

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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- protein search, using sw model OM protein October 30, 2004, 01:35:06; Search time 39 Seconds (without alignments) 471.215 Million cell updates/sec Run on:

US-09-084-691B-206 1045 1 MSTLPKPQRKTKRNTNRRPT......CSFSIFLIALLSCLTTPASA 191 Perfect score:

Scoring table: Sequence:

283416 seqs, 96216763 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
!: pir4:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

2	Description	qenome polyprotein		genome polyprotein	genome polyprotein	hypothetical prote	genome polyprotein				genome polyprotein		genome polyprotein		genome polyprotein	polypeptide - hepa	genome polyprotein	genome polyprotein		genome polyprotein	genome polyprotein	genome polyprotein	polyprotein - hepa	genome polyprotein					genome polyprotein	
COLUMNIA	ID	S40770	GNWVCH	S12707	S18031	PN0677	GNWVC3	GNWVCJ	GNWVTC	JH0711	JQ1584	S32740	S19876	PC1284	S19875	PC2219	GNWVTW	S18030	JQ1925	PC2060	A45573	S21471	JQ1926	S18032	S41288	PC2061	JQ0883	A44150	JQ0881	J01303
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	å Query Match Length	3011	3011	441	782	787	3011	3010	3010	550	640	189	782	513	782	876	3010	3010	520	411	3010	369	523	782	492	411	874	513	874	3033
æ	Query Match	93.5	93.4	92.9	92.7	92.7	95.6	92.3	92.3	92.1	95.0	91.8	91.7	91.6	91.6	91.6	91.5	91.5	91.1	91.0	90.7	90.6	90.6	90.6	90.5	90.3	90.0	0.06	6	89.9
	Score	977	916	971	696	696	968	965	365	962	961	959	958	957	957	957	926	926	952	951	948	947	947	947	946	944	941	940	939	939
	Result No.	1	8	m	4	S	9	7	89	9	10	11	12	13	14	15	16	17	18		20	21	22	23	24	25	26	27	28	29

| genome polyprotein |
|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|
| | | | | | | | | | | | | | | | |
| GNWVJB | PS0388 | JN0265 | JC5620 | S41360 | 841361 | PQ0393 | S41346 | 841362 | S41363 | 841345 | S41364 | S41365 | S41366 | S41344 | 841358 |
| 1 GNWVJB | 2 PS0388 | 2 JN0265 | 1 JC5620 | 2 S41360 | 2 841361 | 2 PQ0393 | 2 S41346 | 2 S41362 | 2 S41363 | 2 S41345 | 2 S41364 | 2 \$41365 | 2 \$41366 | 2 S41344 | 2 \$41358 |
| - | 7 | ~ | | 124 2 S41360 | ~ | 7 | 7 | 7 | ~ | 03 | ~ | α | 03 | 03 | 07 |
| 3033 1 (| 178 2 1 | 322 2 | 3014 1 | ~1 | 123 2 8 | 266 2 1 | 118 2 8 | 114 2 8 | 117 2 8 | 115 2 8 | 115 2 8 | 114 2 8 | 114 2 8 | 115 2 8 | 114 2 8 |
| 89.6 3033 1 (| 87.9 178 2 1 | 87.8 322 2 | 85.5 3014 1 | 124 2 8 | 60.8 123 2 8 | 60.4 266 2 1 | 59.9 118 2 8 | 59.0 114 2 8 | 58.6 117 2 8 | 58.5 115 2 8 | 58.4 115 2 8 | 58.3 114 2 8 | 57.9 114 2 8 | 57.9 115 2 8 | 57.8 114 2 8 |

ALIGNMENTS

RESULT 1

840770	
genome polyprotein - hepatitis C virus	
N; Contains: capsid protein C; envelope protein M; hepacivirin (EC 3.4.21.98) (nonstr	astr
protein NS4a; nonstructural protein NS4b; nonstructural protein NS5	
C;Species: hepatitis C virus	
C;Date: 19-May-2000 #sequence revision 19-May-2000 #text change 09-Jul-2004	
Leading and a second and a second as a sec	

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C; Accession: S40770; PC1285 R; Okamoto. H

R;OKamoto, H. submitted to the EMBL Data Library, March 1992 Reference number: S40770 A;Accession: S40770

A; Molecule type: genomic RNA A; Residues: 1-3011 <0KA> A; Cross-references: UNIPROT: Q03463; EMBL: D10749; NID: g221586; PIDN: BAA01582.1; PID: g2215 A; Cross-references: UNIPROT: Q03463; EMBL: D10749; NID: g221586; PIDN: BAA01582.1; PID: g2215 B; Okamoto, H.; Okada, S.; Sugiyama, Y.; Yotsumoto, S.; Tanaka, T.; Yoshizawa, H.; Tsuda, Jpn. J. Exp. Med. 60, 167-177, 1990 Jpn. J. Exp. Med. 60, 167-177, 1990 A; Title: The S'-terminal sequence of the hepatitis C virus genome. A; Reference number: PC1284; MUID: 91013116; PMID: 2170712

A; Molecule type: genomic RNA
A; Molecule type: genomic RNA
A; Residues: 1-513 < 0K2>
A; Cross-references GB: D00831; NID: 9221511; PIDN: BAA00705.1; PID: 9221512
A; Cross-references GB: D00831; NID: 9221511; PIDN: BAA00705.1; PID: 9221512
A; Experimental source: 1solate HC-J1
C; Superfamily: hepatitis C virus genome polyprotein
C; Keywords: ATP; glycoprotein; hydrolase; nucleotide binding; P-loop; polyprotein; c; Keywords: ATP; product: apsid protein C #status predicted < CPC>
F: 116-191/Product: major envelope protein B #status predicted < NED>
F: 192-389/Product: major envelope protein NS #status predicted < NSD>
F: 30-1006/Product: nonstructural protein NS2 #status predicted < NS2>
F: 100-1615/Product: hepatoivirin #status predicted < NS2>
F: 100-1615/Product: nonstructural protein NS2 #status predicted < NS2>
F: 130-1237/Region: nucleotide-binding motif B
F: 1312-1317/Region: nucleotide-binding motif B

F:1316-1319/Region: DEXH motif F:1616-1862/Product: nonstructural protein NS4a #status predicted <N4A. F:1863-2013/Product: nonstructural protein NS4b #status predicted <N4B. F:2014-3011/Product: nonstructural protein NS5 #status predicted <NS5>

<N4A>

Gaps 0; Length 3011; / Match 93.5%; Score 977; DB 1; Length 30 Local Similarity 92.1%; Pred. No. 2.9e-74; Pred. No. 2.9e-74; Pred. S. Mismatches 9; Indels Query Match Best Local S: Matches 176,

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09 1 MSTLPKPQRKTKRNTNRRPTDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRG

1 MSTIPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRG 60

RRQPIPKARQPQGRHWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPHWGPNDPRRRSRNLG 120

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Gaps

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C; Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C; Accession: S12707
C; Accession: S12707
C; Accession: S12707
Nucleic Acids Res. 18, 4626, 1990
A; Title: Nucleotide sequence of core and envelope genes of the hepatitis C virus genome A; Reference number: S12707; MUID: 90356432; PMID: 2117749
A; Accession: S12707
A; Molecule type: genomic RNA
A; Residues: 1-441 < TAK>
                                                                                                                                                                                                                                                                          A;Cross-references: UNIPROT:081776; EMBL:D00574; NID:g221656; PIDN:BAA00452.1; PID:g221
C;Superfamily: hepatitis C virus genome polyprotein
C;Keywords: polyprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Supering polyprotein - hepatitis C virus (isolate JK2) (fragment)

N;Contains: core protein; envelope protein 1; nonstructural protein 2; NS1/E2 protein

N;Contains: core protein; envelope protein 1; nonstructural protein 2; NS1/E2 protein

A;Variety: isolate JK2

C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004

C;Bupition: Sequence analysis of putative structural regions of Hepatitis C Virus is

A;Molecule type: genomic RNA

A;Reference number: S18039

A;Molecule type: genomic RNA

A;Residues: 1-782 cHON>

A;Cross-references: UNIPROT: Q68950; EMBL:X61593

A;Experimental source: isolate JK2

C;Superfamily: hepatitis C virus gredicted AMAT1>

C;Superfamily: hepatitis C virus gredicted AMAT2>

F;192-383/Product: core protein; metatus predicted AMAT3>

F;192-383/Product: Nonstructural protein 2 (fragment) #status predicted AMAT3>

F;734-782/Product: nonstructural protein 2 (fragment) #status predicted AMAT3>
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                                                                                                                                                                                                                                                                                                                                                                                                                       Score 971; DB 2; Length 44
Pred. No. 1.5e-74;
5; Mismatches 9; Indels
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92.7%;
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Best Local Similarity 92.7
Matches 177; Conservative
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AyNote: neither amino acid nor nucleotide sequence is given
C;Superfamily: hepatitis C virus genome polyprotein
C;Superfamily: hepatitis C virus genome polyprotein
C;Superdas: AFP; capsid protein; envelope proteinin; glycoprotein; hydrolase; nonstructura
F;116-191/Product: capsid protein M #status predicted <CPC>
F;116-191/Product: envelope protein B #status predicted <MBE>
F;390-729/Product: monstructural protein NS1 #status predicted <NS2>
F;1007-1615/Product: nonstructural protein NS2 #status predicted <NS2>
F;1007-1615/Product: honstructural protein NS2 #status predicted <NS2>
F;1230-1237/Region: nucleotide-binding motif A (P-loop)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              F;1616-1862/Product: nonstructural protein NS4a #status predicted <N4A>
F;1683-2013/Product: nonstructural protein NS4b #status predicted <N4B>
F;2014-3011/Product: nonstructural protein NS5 #status predicted <NS5>
F;2014-3011/Product: nonstructural protein NS5 #status predicted <NS5>
F;196,209,234,305,325,417,423,430,448,476,532,540,556,576,623,645,1213,1255,2041,2240,23
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A, Residues: 1-3011 <INC>
A, Residues: 1-3011 <INC>
A, Cross-references: UNIPROT: D27958; GB: M67463; NID: G329737; PIDN: AAA45534.1; PID: G329738
R, Inchauspe, G.; Zebedee, S.; Lee, D.H.; Sugitani, M.; Nasoff, M.; Prince, A.M.
Proc. Natl. Acad. Sci. U.S.A. 88, 10292-10296, 1991
A, Title: Genomic structure of the human prototype strain H of hepatitis C virus: compari
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C,Accession: A36814, A41546 - K; Lee, D.H.; Sugitani, M.; Nasoff, M.; Prince, A.M. R;Inchauspe, G, Zebedee, S.; Lee, D.H.; Sugitani, M.; Nasoff, M.; Prince, A.M. submitted to GenBank, July 1992 A;Description: Genomic structure of the human prototype strain H of hepatitis C virus:
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                                                                                                                                                                                                                                                                                                                              genome polyprotein - hepatitis C virus (strain H)
N;Contains: capsid protein C; envelope protein M; hepacivirin (EC 3.4.21.98)
protein NS4a; nonstructural protein NS4b; nonstructural protein NS5
                                                                                                                                                                                                                                                                                                                                                                                                                Cypecies: hepatitis C virus
A;Note: host Homo sapiens (man)
C;Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 09-Jul-2004
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A,Contents: annotation
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Best Local Similarity 92.7
Matches 177; Conservative
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|LLSCLTVPASA 191
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                                                                                                            LLSCLTTPASA
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A; Residues: 1577-1633 < CH2>
A; Experimental source: isolates B-b17
C; Superimental source: isolates B-b17
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C;Species: hepatitis C virus
C;Species: hepatitis C virus
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
R;Kato, N.; Hijkata, M.; Ootsuyama, Y.; Nakagawa, M.; Ohkoshi, S.; Sugimura, T.; Shimot
R;Recession: A39233 MUD:91088550; PMID:2175903
A;Recession: A39233 MUD:91088550; PMID:2175903
A;Residues: 1-3010 KATA
A;Residues: 1-3010 KATA
A;Residues: UMPROT:P26662; GB:D90208; NID:G221610; PIDN:BAA14233.1; PID:G221611
R;Kato, N.; Obkoshi, S.; Shimotobno, K.
Proc. Jpn. Acad. 65B, 219-223, 1989
A;Title: Japanese isolates of the non-A, non-B hepatitis viral genome show sequence vari
A;Reference number: PS0085
A;Reference number: PS0086
A;Molecule type: genomic RNA
A;Residues: 2650-2707 KA2>
A;Experimental source: Japanese isolate
C;Comment: The cleavage sites of this polyprotein have not been determined.
C;Superfamily: hepatitis C virus genome polyprotein
C;Keywords: ATF; glycoprotein; hydrolase; nucleotide binding; P-loop; polyprotein; R-116,1941/P-ndurt: envelone predicted cRPO>
R:116,1941/P-ndurt: envelone protein M #starus predicted cRPO>
R:116,1941/P-ndurt envelone protein M #starus predicted cRPO>
R:116,1941/P-ndurt envelone protein R:116,1941/P-ndurt envelone
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N.Contains: capsid protein C; envelope protein M; major envelope protein E; nonstructura
protein NS4a; nonstructural protein NS4b; nonstructural protein NS5
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F;116-1917Product: envelope protein M #status predicted <EPM>
F;192-389/Product: major envelope protein E #status predicted <MSE>
F;390-729/Product: nonstructural protein NSI #status predicted <NSI>
F;730-1006/Product: nonstructural protein NS2 #status predicted <NS2>
F;1007-1615/Product: hepacivirin #status predicted <NS3>
F;1230-1237/Region: nucleotide-binding motif A (P-loop)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .
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al Similarity 91.6%;
175; Conservative 6
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N; Contains: capsid protein C; envelope protein M; hepacivirin (EC 3.4.21.98) (nonstructu
N; Contains: capsid protein C; envelope protein M; hepacivirin (EC 3.4.21.98) (nonstructu
N; Contains: capsid protein C; envelope protein NS5
C; Species: hepatitis C virus
C; Species: hepatitis C virus
C; Date: 30-8ep-1992 #sequence revision 30-8ep-1992 #text_change 09-Jul-2004
C; Accession: A39166; D00403; P00404
R; Choo, Q.L.; Richman, K.H.; Han, J.H.; Berger, K.; Lee, C.; Dong, C.; Gallegos, C.; Coi
Proc. Natl. Acad. Sci. U.S.A. 88, 2451-2455, 1991
A; Title: Genetic organization and diversity of the hepatitis C virus.
A; Reference number: A39166; MUID: 91172826; PMID: 1848704
A; Residues: 1-3011 < Choo.
A; Cross-references: UNIPROT: 226664; GB: M62321; NID: 9329873; PIDN: AAA45676.1; PID: 9329874
B; Chan, S.W.; McOmish, F.; Holmes, E.C.; Dow, B.; Peutherer, J.F.; Follett, E.; Yap, P.L
J. Gen. Virol. 73, 1131-1141, 1992
A; Title: Analysis of a new hepatitis C virus type and its phylogenetic relationship to e
A; Reference number: PQ0393; MUID: 92268871; PMID: 1316939
A; Accession: PQ0403
A; Cross-references: 1577-1633 < CHA>
A; Residues: 1-377-1633 < CHA>
A; Residues: 1-377-163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A,Cross-references: UNIPROT:008244, GB:L20498, NID:g1381031, PIDN:AAB02608.1; PID:g13810
C;Superfamily: hepatitis C virus genome polyprotein
C;Roywords: glycoprotein; nonstructural protein
F;196,209,234,250,305,325,421,427,452,536,544,560,580,627,649/Binding site: carbohydrate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gen
                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein 787 - hepatitis C virus (fragment)
C;Species: hepatitis C virus
C;Date: 14-Jul-1994 #sequence_revision 14-Jul-1994 #text_change 09-Jul-2004
C;Accession: PN0677
R;Cho, S.H.; Yoon, J.I.; Chang, J.E.; Ahn, B.M.; Lee, C.H.; Lee, Y.I.
Blochem. Bloc
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Pred. No. 3.8e-74;
4; Mismatches 10;
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Best Local Similarity 92.7%;
Matches 177; Conservative
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A; Residues: 1-787 < CHO>
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us-09-084-691b-206.rpr

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Genome polyprotein - hepatitis C virus (strain PRC1) (fragments)

N;Contains: envelope protein E1; envelope protein E2; nonstructural protein NS1; nonstructuralis: envelope protein E1; envelope protein E2; nonstructural protein NS1; nonstructural protein NS1; nonstructural protein NS1; nonstructural protein NS2, consession: JH0711

R;Liu, K.; Hu, Z.; Li, H.; Prince, A.M.; Inchauspe, G.
Gene 114, 245-250, 1992

A;Title: Genomic typing of hepatitis C viruses present in China.

A;Reference number: JH0711; MUDD: 92290283; PMID: 1318245

A;Reference number: JH0711; MUDD: 92290283; PMID: 1318245

A;Residues: 1-550 cLIU>
A;Residues: 1-500 cLIU>
A;Residues: 1-550 cLIU>
A;Residu
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N;Contains: core protein C; envelope protein E1; envelope protein E2; nonstructural prote C;Species: hepatitis C virus
C;Species: hepatitis C virus
C;Species: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 09-Jul-2004
C;Accession: JQ1584
R;Kumar, U.; Chang, D.; Thomas, H.; Monjardino, J.
J; Gen. Virol. 73, 1241-1525, 1992
A;Title: Cloning and sequencing of the structural region and expression of putative corrections of sequencing of the structural region and expression of putative corrections of the structural region and expression of putative corrections of the structural region and expression of putative corrections of Superfamily: Pulp. 92300349; PMID:1318944
A;Residues: 1-640 «KUNA
A;Cross-references: UMIPROT:Q68966; GB:X84079; NID:G643119; PIDN:CAA58888.1; PID:G64312C
C;Superfamily: hepatitis C virus genome polyprotein
C;Superfamily: hepatitis C virus genome polyprotein
C;Superfamily: hepatitis C virus genome polyprotein
C;Superfamily: hepatitis C virus genome polyprotein; nonstructural protein; polyprote; H;192-389/Product: core protein E1 #status predicted «EE1>
KVIDTLICGFADIMGYIPLVGAPLGGAARALAHGVRVLEDGVYYATGNLPGCSFSIFLA 180
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Best Local Similarity 91.6%;
Matches 175; Conservative
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C'Superfamily: hepatitis C virus genome polyprotein

C'Supersonas: AFP; capsid protein; envelope protein; glycoprotein; hydrolase; nonstructura

C'2-115/Product: capsid protein C #status predicted <CPC>

F;116-191/Product: envelope protein M #status predicted <CPC>

F;192-389/Product: major envelope protein B #status predicted <NEB>

F;390-729/Product: major envelope protein MS1 #status predicted <NS1>

F;730-1006/Product: nonstructural protein NS2 #status predicted <NS2>

F;1007-1615/Product: nonstructural protein NS2 #status predicted <NS2>

F;1007-1615/Product: nonstructural protein MS2 #status predicted <NS2>

F;11310-1317/Region: nucleotide-binding motif A (P-loop)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 F;196,209,234,250,305,325,417,423,430,448,532,540,556,576,623,645,1213,1255,2041,2077,24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Accession: A38465
R;Takamizawa, A.; Mori, C.; Fuke, I.; Manabe, S.; Murakami, S.; Fujita, J.; Onishi, E.;
Virol. 65, 1105-1113, 1991
A;Title: Structure and organization of the hepatitis C virus genome isolated from human A;Reference number: A38465; MUID:91140698; PMID:1847440
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A,Residues: 1-3010 <TAK>
A;Cross-references: UNIPROT:P26663; EMBL:M58335; NID:g329770; PIDN:AAA72945.1; PID:g3297
                                                                                  F;1616-1862/Product: nonstructural protein NS4a #status predicted <N4A>
F;1863-2013/Product: nonstructural protein NS4b #status predicted <N4B>
F;2014-3010/Product: nonstructural protein NS5 #status predicted <NS5>
F;2014-3010/Product: nonstructural protein NS5 #status predicted <NS5>
F;196,209,234,250,305,325,411,423,430,448,532,556,576,625,645,1213,1255,2041,2077,2240,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MSTNPKPQRKTKRNTNRRPQDVKFPGGGOIVGGVYLLPRRGPRLGVRAPRKTSBRSQPRG
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Pred. No. 2.9e-73;
5; Mismatches 10; Indels
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Pred. No. 2.9e-73;
5; Mismatches 10; Indels
   nucleotide-binding motif
DEXH motif
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92.1%;
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Best Local Similarity 92.1%;
Matches 176; Conservative
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LLSCLTIPASA 191
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Best Local Similarity
Matches 176; Conserv
                                                   ;1316-1319/Region:
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R;Honda, M.; Kaneko, S.; Masashi, U.; Kobayashi, K.; Murakami, S.
submitted to the EMBL Data Library, September 1991
A;Description: Sequence analysis of putative structural regions of Hepatitis C Virus iso
A;Reference number: S18029
A;Reference number: S18029
A;Accession: S19876
A;Molecule type: genomic RNA
A;Residues: 1-782 < HON>
A;Residues: 1-782 < HON>
A;Residues: 1-782 < HON>
A;Cross-references: UNIPROT:Q68953; EMBL:X61595; NID:g59486; PIDN:CAA43792.1; PID:g59487
A;Experimental source: isolate JKS
C;Superimental source: isolate JKS
C;Superimental source: isolate JKS
C;Superimental source: isolate JKS
F;1-191/Product: core protein; envelope protein; glycoprotein; nonstructural
F;1-191/Product: core protein #status predicted < MAT2>
F;192-383/Product: envelope protein # #status predicted < MAT3>
F;34-733/Product: nonstructural protein 2 (fragment) #status predicted < MAT4>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            genome polyprotein - hepatitis C virus (isolate HC-J4) (fragment)
C;Species: hepatitis C virus
C;Species: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C;Date: 30-Sep-1993
Rsequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C;Accession: PC1284
R;Okamoto, H.; Okada, S.; Sugiyama, Y.; Yotsumoto, S.; Tanaka, T.; Yoshizawa, H.; Tsuda, Jpn. J. Exp. Med. 60, 167-177, 1990
A;Aritle: The S'-terminal sequence of the hepatitis C virus genome.
A;Reference number: PC1284; MUID:91013116; PMID:2170712
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A,Residues: 1-513 <OKA>
A,Cross-references: UNIPROT:Q81221; GB:D00832; NID:g221513; PIDN:BAA00706.1; PID:g221514
C,Superfamily: hepatitis C virus genome polyprotein
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Pred. No. 3.2e-73;
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Pred. No. 2.6e-73;
5; Mismatches 11
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91.6%;
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91.6%;
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Matches 175; Conservative
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Best Local S:
Matches 175,
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       F;390-640/Product: envelope protein E2 and nonstructural protein NS1 #status predicted < F;196,209,234,305,417,430,448,476,540,556,576,623/Binding site: carbohydrate (Asn) (cova
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N;Contains: core protein; envelope protein 1; nonstructural protein 2; NS1/E2 C;Species: hepatitis C virus
A;Variety: isolate JKS
C;Date: 30-Unn-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
C;Accession: S19876
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N;Contains: capsid protein C; envelope protein M
N;Contains: capsid protein C; envelope protein M
C;Species: hepatitis C virus
C;Date: 19-Mar-1997 #sequence_revision 05-Dec-1998 #text_change 09-Jul-20
C;Accession: 532740
R;Vassilev, V.B.; Viazov, S.O.; Kotova, E.Y.; Nosikov, V.V.
submitted to the EMBL Data Library, April 1993
A;Description: Evidence of new HCV variant of European isolate in Russia.
A;Reference number: 532740
A;Molecule type: genomic RNA
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Pred. No. 6.9e-74;
5; Mismatches 10; Indels
                                                                          Length 640;
                                                                                                                       11; Indels
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C; Superfamily: hepartitis C virus genome polyprotein
C; Keywords: capsid protein; envelope protein; polyprotein
F; 1-11s/Product: capsid protein C #status predicted <CPC>F; 116-189/Product: envelope protein M #status predicted <EPM>
                                                                       Score 961; DB 2;
Pred. No. 1.5e-73;
                                                                                                                     6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 92.1%;
Matches 174; Conservative
                                                                       Query Match
Best Local Similarity 91.1%;
Matches 174; Conservative
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                                          genome polyprotein - hepatitis C virus (isolate JK3) (fragment)

N;Contains: core protein; envelope protein 1; nonstructural protein 2; NS1/E2 protein
C;Species: hepatitis C virus
A;Variety: isolate JK3
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
C;Accession: S19875
R;Honda, M.; Kaneko, S.; Masashi, U.; Kobayashi, K.; Murakami, S.
submitted to the EMBL Data Library, September 1991
A;Deference mumber: S18029
A;Accession: Sequence analysis of putative structural regions of Hepatitis C Virus isola;A;Reference mumber: S18029
A;Accession: S19875
A;Accession: S19875
A;Accession: S19875
A;Accession: Sequence analysis of putative structural regions of Hepatitis C Virus isola;A;Residues: 1-782 4HON>
A;Residues: 1-782 4HON>
A;Cross-references: UNIPROT: Q68951; EMBL: X61592; NID: G59482; PIDN: CAA43789.1; PID: G59483
A;Cross-references: UNIPROT: Q68951; EMBL: X61592; NID: G59482; PIDN: CAA43789.1; PID: G;Superfamily: hepatitis C virus genome polyprotein
C;Keywords: capsid protein; core protein; envelope protein; myllocaticed AMAI2>
F;192-383/Product: core protein #status predicted AMAI2>
F;192-383/Product: NS1/E2 protein #status predicted AMAI2>
F;384-733/Product: NS1/E2 protein #status predicted AMAI3>
F;734-782/Product: nonstructural protein 2 (fragment) #status predicted AMAI4>
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N.Contains: core protein; B1 (carboxyl end); B2/NS1 (amino end); NS3 protein; NS4A prote
C.Species: hepatitis C virus
C.Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
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A;Residues: 1-876 <STU>
A;Cross-references: UNIPROT:Q81242; GB:L29577; GB:L29579;
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Fil-19-1/Product: core #status predicted <COE>
Fig-19-12/Product: core #status predicted <COE>
Fig-247/Product: El (carboxyl end) #status predicted <ERE>
Fig-24-41/Product: El (samino end) #status predicted <ERE>
Fig-348-318/Region: NSI (amino end)
Fig-319-411/Region: NSI (amino end)
Fig-319-781/Product: NSI #status predicted <NSR>
Fig-38-7Product: NSI #status predicted <NSR>
Fig-38-876/Product: NSI #status predicted <NSB>
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ilarity 91.6%; Pred. No. 3.9e-73;
Conservative 5; Mismatches 11;
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Best Local Simi
Matches 175;
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RESULT 14
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F;281,287,294,312,340/Binding site: carbohydrate (Asn) (covalent) #status predicted
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0
                                                   Length 876;
                                                                                                 11; Indels
                                                Score 957; DB 2;
Pred. No. 4.4e-73;
8; Mismatches 11;
                                                   91.6%;
ilarity 90.1%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                               181 LLSCLTTPASA 191
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                                                     Query Match
Best Local Similarity
Matches 172; Conserv
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RRQPIPKARQPQGRHWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPHWGPNDPRRRSRNLG 120
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Hepatitis C virus.
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NCBI_TaxID=11103;
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Q68115;
01-NOV-1996 (
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01-JUN-2003
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SEQUENCE
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563.572 Million cell updates/sec
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1045
1 MSTLPKFQRKTKRNTNRRPT......CSFSIFLLALLSCLTTPASA 191
                                                                                                                              October 30, 2004, 01:34:01 ; Search time 195 Seconds
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                  version 5.1.6
- 2004 Compugen Ltd.
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Maximum Match 1008
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Gapop 10.0 , Gapext 0.5
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2: uniprot_trembl:*
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Q81267 hepatitis c
Q6x147 hepatitis c
Aap6953 hepatitis c
P87841 hepatitis c
Q81274 hepatitis c
Q81274 hepatitis c
Q81273 hepatitis c
Q68157 hepatitis c
Q68157 hepatitis c
Q68157 hepatitis c
Q68116 hepatitis c
Q68116 hepatitis c
Q68116 hepatitis c
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MEDLINE=92279243; PubMed=1317578;
Bukh J., Purcell R.H., Miler R.H.;
"Sequence analysis of the 5' noncoding region of hepatitis C virus.";
Proc. Natl. Acad. Sci. U.S.A. 89:4942-4946(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-933'6778, N. H. Miller R.H.;

Bukh J., Purcell R.H., Miller R.H.;

Bukh J., Purcell R.H., Miller R.H.;

"At least I genotypes of hepatitis C virus predicted by sequence analysis of the putative E1 gene of isolates collected worldwide.";

Proc. Natl. Acad. Sci. U.S.A. 90.8234-8238 (1993).

EMBL, U10198; AAA21037.1; -.

GO; GO:001902; C:viral capsid, IEA.

GO; GO:001902; F:structural molecule activity; IEA.

InterPro; IPR00252; HCV capsid.

InterPro; IPR00251; HCV capsid.

Pfam; PF01543; HCV capsid.

Pfam; PF01542; HCV_core;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
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SEQUENCE FROM N.A.
BURDILNES-84336721; PubMed=8058787;
Bukh J., Purcell R.H., Miller R.H.;
"Sequence analysis of the core gene of 14 hepatitis C virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7A7994DF2F0909C6 CRC64;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         genotypes.";
Proc. Natl. Acad. Sci. U.S.A. 91:8239-8243(1994)
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                    Q6XJ47
AAP69953
O92529
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Q81274
Q39647
Q68698
Q681273
Q68152
Q68157
Q68105
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DB 2; Length 191;

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P89958;
01-MAY-1997 (TrEMBLrel. 03, Created)
01-MAY-1997 (TrEMBLrel. 03, Last seg
01-JUN-2003 (TrEMBLrel. 24, Last ann
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                                                                                                                                                  EMBL; D88469; BAA13618.1; -. PIR; PQ0804; PQ0804.
                                                                                                                                                                                                                                                                                                                                                                                                           98.18;
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Best Local Similarity
Matches 187; Conserv
[1]
SEQUENCE FROM N.A.
                                                                                                                   SEQUENCE FROM N.A.
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NCBI_TaxID=11103;
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                           KVIDTLTCGFADLMGYIPVVGAPLGGVAAALAHGVRAIEDGINYATGNLPGCSFSIFLLA 180
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                                                                                                                                                                                                                                                                                                                              MEDIINE=97052554; PubMed=8897188;
Bernier L., Willems B., Delage G., Murphy D.G.;
"Identification of numerous hepatitis C virus genotypes in Montreal,
                                                                                                                                                                                     01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Core protein (Fragment).
Hepatitis C virus type 6.
Hepatitis C virus type 6.
Hepatitis RNA positive-strand viruses, no DNA stage; Flaviviridae;
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Hepatitis C virus.
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Hepacivirus.
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Last annotation update)
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Pred. No. 4.8e-79;
0; Mismatches 2;
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                                                                                                PRELIMINARY;
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R GO; GO:0019021; C:integral to membarane; IEA.

R GO; GO:0019028; C:viral capsid; IEA.

GO; GO:0019018; C:viral envelope; IEA.

GO; GO:0019018; F:seructural molecule activity; IEA.

R InterPro; IPR002521; HCV_core.

R InterPro; IPR002521; HCV_core.

R InterPro; IPR002531; HCV_core.

R InterPro; IPR002531; HCV_core.

R Pfam; PF01543; HCV_core; I.

R Pfam; PF01543; HCV_core; I.

R Pfam; PF01543; HCV_core; I.

R Pfam; PF01559; HCV_core; I.

R Pfam; PF01569; HCV_core; I.

R Pfam; PF01560; HCV_core; I.
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01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
core, env and part of B2/NS1 (Fragment).
Hepatitis C virus.
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tokita H., Okamoto H., Tsuda F., Song P., Nakata S., Chosa T., Iizuka H., Mishiro S., Miyakawa Y., Mayumi M.; "Hepatitis C virus variants from Vietnam are classifiable into the seventh, eighth, and ninth major genetic groups."; Proc. Natl. Acad. Sci. U.S.A. 91:11022-11026 [1994].
MEDILINE=95662197; PubMed=7972001;
Tokita H., Okamoto H., Tsuda F., Song P., Nakata S., Chosa T.,
Tizuka H., Mishiro S., Miyakawa Y., Mayumi M.;
"Hepatitis C virus variants frow Vietnam are classifiable into the seventh, eighth, and ninth major genetic groups.";
Proc. Natl. Acad. Sci. U.S.A. 91:11022-11026(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
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                                                                                                                                                                                                                                                                                                                Okamoto H.;
Submitted (AUG-1996) to the EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 1025; DB 2;
Pred. No. 7.3e-78;
1; Mismatches 3;
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61 RRQPIPKARQPQGRHWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPHWGPNDPRRRSRNIG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                61 RRÓPIPKARQSGGRHWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPNWGPNDPRRRSRNLG 120
                                                                                                                                                                                                                                                                                                                      1 MSTLPKPQRKTKRNTNRRPTDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRG 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "The entire nucleotide sequences of three hepatitis C virus isolates in genetic groups 7-9 and comparison with those in the other eight genetic groups.";

J. Gen. Virol. 79:1847-1857(1998).

EMBL; D84264; BAA32666.1; -.
InterPro; IPR002521; HCV core.
InterPro; IPR002519; HCV env.
InterPro; IPR002511; HCV env.
InterPro; IPR002531; HCV appid; 1.
Pfam; PP01542; HCV core; 1.
Pfam; PP01542; HCV core; 1.
Pfam; PP01560; HCV env; 1.
Coat protein; Envelope protein; Glycoprotein; Nonstructural protein; NoN_TER 414 414
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0016021; C:viral capsid; IEA.
GO; GO:0019031; C:viral capsid; IEA.
GO; GO:0019031; C:viral envelope; IEA.
GO; GO:000524; F:ATP-binding; IEA.
GO; GO:0000252; F:ATP-dependent helicase activity; IEA.
GO; GO:0000358; F:RNA-directed RNA polymerase activity; IEA.
GO; GO:0000358; F:serine-type peptidase activity; IEA.
GO; GO:000508; F:serine-type peptidase activity; IEA.
GO; GO:000508; F:strine-type peptidase activity; IEA.
GO; GO:000508; F:strine-type peptidase activity; IEA.
GO; GO:000508; F:protecolysis and peptidolysis; IEA.
GO; GO:0010909; P:viral genome replication; IEA.
InterPro; IPRO00345; CytC_heme_BS.
                                                                                                                                                                                                                                            Length 414;
                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                      CRC64;
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Last annotation update)
                                                                                                                                                                                                                                        Score 1024; DB 2;
Pred. No. 8.8e-78;
1; Mismatches 2;
                                                                                                                                                                                                    65355640863B3DCF
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                                                                                                                                                                                                      414 AA; 44937 MW;
                                                                                                                                                                                                                                        98.0%;
98.4%;
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                                                                                                                                                                                                                                                                                Matches 188; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181 LLSCLTTPASA 191
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HSSP; P27958; 1A1V.
                                                                                                                                                                                                                                                              Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEROPS; S29.001; -.
MEROPS; U39.001; -.
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                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 RRQPIPKARQPTGRHWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPHWGPNDPRRRSRNLG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KVIDTLTCGFADLMGYIPVVGAPLGGVAAALAHGVRAIEDGINYATGNLPGCSFSIFLLA 180
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DR GO; GO:0016021; C:integral to membrane; IEA.

DR GO; GO:0019028; C:viral capsid; IEA.

DR GO; GO:0019021; C:viral envelope; IEA.

BG GO; GO:005198; P:structural molecule activity; IEA.

DR GO; GO:005198; P:structural molecule activity; IEA.

BR InterPro; IPR00252; HCV capsid.

BR InterPro; IPR002521; HCV env.

BR InterPro; IPR002531; HCV env.

BR Ffam; PF01542; HCV corp.

BR Pfam; PF01542; HCV corp.

BR Pfam; PF01560; HCV NS1; 1.

BR Pfam; PF01560; HCV NS1; 1.
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MEDLINE=95062197; PubMed=7972001;
Tokita H., Okamoto H., Tsuda F., Song P., Nakata S., Chosa T.,
Tizuka H., Mishiro S., Miyakawa Y., Mayumi M.;
"Hepatitis C virus variants from Vietnam are classifiable into the seventh, eighth, and ninth major genetic groups.";
Proc. Natl. Acad. Sci. U.S.A. 91:11022-11026(1994).
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Okamoto H.;
Submitted (AUG-1996) to the EMBL/GenBank/DDBJ databases.
EMBL; D88468; BAA13617.1; -.
FIR; PQ0804, PQ0804.
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0019028; C:riral capsid; IEA.
GO; GO:0019011; C:viral envelope; IEA.
GO; GO:0019011; C:viral envelope; IEA.
IEA.
GO; GO:005198; F:structural molecule activity; IEA.
InterPro; IPR002522; HCV_capsid.
                                  Okamoto H.;
Submitted (AUG-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                              414 AA; 44973 MW; F3F3CF154372F4FF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                              Score 1024; DB 2;
Pred. No. 8.8e-78;
2; Mismatches 3;
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Hepatitis C virus.
                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 98.0%;
Best Local Similarity 97.4%;
Matches 186; Conservative
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              SEQUENCE FROM N.A.
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61 RRQPIPKARQPQGRHWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPHWGPNDPRRRSRNLG 120
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Coat protein; Envelope protein; Glycoprotein; Nonstructural protein;
Polyprotein; Transmembrane.
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                R GO; GO:0016021, C:integral to membrane; IEA.

R GO; GO:0019028; C:viral capsid; IEA.

GO; GO:0019028; C:viral capsid; IEA.

R GO; GO:0019028; C:viral binding; IEA.

R GO; GO:0008026; F:ATP binding; IEA.

R GO; GO:0008129; F:RNA binding; IEA.

R GO; GO:0008218; F:RNA directed RNA polymerase activity; IEA.

R GO; GO:0008218; F:serine-type peptidase activity; IEA.

R GO; GO:0008318; F:serine-type peptidase activity; IEA.

R GO; GO:0019087; F:serine-type peptidalysis; IEA.

R GO; GO:0019087; P:viral genome replication; IEA.

R InterPro; IPR000345; CytC heme_BS.

R InterPro; IPR0001410; IEA.

R InterPro; IPR0001410; IEA.
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01-MAY-1997 (TrEMBLrel. 03, Created)
01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
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2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR001252; HCV capsid.
InterPro; IPR002521; HCV capsid.
InterPro; IPR002521; HCV core.
InterPro; IPR002519; HCV env.
InterPro; IPR002519; HCV NS1.
InterPro; IPR001490; HCV NS4.
InterPro; IPR001490; HCV NS5a.
InterPro; IPR00166; HCV NSA.
InterPro; IPR00166; HCV RGRP.
InterPro; IPR00190; Peptidase_S29.
InterPro; IPR00190; Peptidase_S29.
InterPro; IPR007095; RNA_POl_DS_PS.
InterPro; IPR01509; HCV capsid; 1.
Pfam; PP01540; HCV core; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    97.98;
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Matches 187; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SMART; SM00487; DEXDC; 1.
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Best Local
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AC P8
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Coat protein; Envelope protein; Glycoprotein; Nonstructural protein;
Polyprotein; Transmembrane.
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Hepatitis C virus type 6a.
Viruses; sRNA positive-strand viruses, no DNA stage; Flaviviridae;
Hepacivirus; Hepatitis C virus type 6.
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MEDLINE=97320431; PubMed=9177282;
Adams A. (Chamberlain R.W., Taylor L.A., Davidson F., Lin C.K., Simmonds P., Elliot R.M.;
—Complete coding sequence of hepatitis C virus genotype 6a.";
Blochem. Blophys. Res. Commun. 234:393-396 (1997).

BMSC, Y12083; CAA72801.1;
—HSSP; P27958; IAIV.
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01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
      INTERPORT IPROUSES,
INTERPORT IPROUSES,
INTERPORT IPROUSES, HCV_ENV.
INTERPORT IPROUSES, HCV_NSI.
INTERPORT IPROUSES, HCV_NSI.
INTERPORT IPROUSES, HCV_NSA.
INTERPORT IPROUSES, HCV_NSA.
INTERPORT IPROUSES, HCV_NSA.
INTERPORT IPROUSES, PEPT_GAS.
INTERPORT IPROUSONS, PEPT_GAS.
INTERPORT IPROUSONS, PEPT_GAS.
INTERPORT IPROUSONS, PEPT_GAS.
INTERPORT IPROUSONS, RNA_DOL DS_PS.
INTERPORT IPROUSONS, RNA_DOL DS_PS.
INTERPORT IPROUSONS, RNA_DOL DS_PS.
INTERPORT IPROUSONS, RNA_DOL DS_PS.
INTERPORT IPROUSONS, HCV_CAPSI, 1.
DR PÉAN, PFOLSS, HCV_CAPSI, 1.
DR PÉAN, PFOLSS, HCV_NSS, 1.
DR PÉAN, PFOLSS, HCV_NSS, 1.
DR PÉAN, PFOLSON, HCV_NSS, 1.
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IPR002522;
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61 RROPIPKAROPIGREWAQPGYAWPLYGNEGCGWAGWLLSPRGSRPHWGPNDFRRSRNLG 120
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                                                                                                                                                                                                                     DR GO, GO.0016021; C.integral to membrane; IEA.

DR GO, GO.0016021; C.integral to membrane; IEA.

DR GO; GO.0016021; C.integral to membrane; IEA.

GO; GO.0016021; C.integral to membrane; IEA.

DR GO; GO.0019031; C.viral capsid; IEA.

DR GO; GO.0019031; C.viral envelope; IEA.

DR GO; GO.0005198; F. BITUCLUAIN molecule activity; IEA.

INTERPRO; IRR002521; HCV_core.

DR InterPro; IRR0025219; HCV_core.

DR InterPro; IRR0025219; HCV_env.

DR InterPro; IRR0025319; HCV_env.

DR Pfam; PF01543; HCV capsid; 1.

R Pfam; PF01543; HCV core; 1.

DR Pfam; PF01559; HCV core; 1.

DR Pfam; PF01559; HCV core; 1.

DR Pfam; PF01559; HCV core; 1.

DR Pfam; PF01560; HCV_NS1; 1.

DR Pfam; PF01589; HGV env; 1.
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  Tokita H., Okamoto H., Tsuda F., Song P., Nakata S., Chosa T., Ilzuka H., Mishiro S., Miyakawa Y., Mayumi M.; Hepatitis C virus variants from Vietnam are classifiable into the seventh, eighth, and ninth major genetic groups.", Proc. Natl. Acad. Sci. U.S.A. 91:11022-11026 (1994).
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SEQUENCE FROM N.A.

TOKITA H., Okamoto H., Tsuda F., Song P., Nakata S., Chosa T.,

Tokita H., Mishiro S., Miyakawa Y., Mayumi M.;

Ilzuka H., Mishiro S., Miyakawa Y., Mayumi M.;

"Hepatitis C virus variants from Yatenam are classifiable into the seventh, eighth, and ninth major genetic groups.";

Proc. Natl. Acad. Sci. U.S.A. 91:11022-11026(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97.2%; Score 1016; DB 2; Length 414; 96.9%; Pred. No. 4.1e-77; ive 2; Mismatches 4; Indels
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Submitted (AUG-1996) to the EMBL/GenBank/DDBJ databases.
EMBL; D88473; BAA13622.1; -.
                                                                                                                                                                                                          Okamoto H.;
Submitted (AUG-1996) to the EMBL/GenBank/DDBJ databases
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Last annotation update)
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Hepatitis C virus.
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01-MAY-1997 (TrEMBLrel. 03, Last seq
01-OCT-2003 (TrEMBLrel. 25, Last ann
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Matches 185; Conservative
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Polyprotein; Transmembrane.
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                                                                                      Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE=95062197; PubMed=7972001;
Tokita H., Okamoto H., Tsuda F., Song P., Nakata S., Chosa T.,
Tizuka H., Mishiro S., Miyakawa Y., Mayumi M.;
"Hepatitis C virus variants from Vietnam are classifiable into the seventh, eighth, and ninth major genetic groups.";
Proc. Natl. Acad. Sci. U.S.A. 91:11022-11026(1994).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 A Okamoto H.;

Submitted (AUG-1996) to the EMBL/GenBank/DDBJ databases.

EMBL; D88476; BAA13625.1;

R GO; GO:0016021; C:integral to membrane; IEA.

GO; GO:0019028; C:viral capsid; IEA.

GO; GO:0019031; C:viral envelope; IEA.

R GO; GO:0005198; F:structural molecule activity; IEA.

InterPro; IPR005121; HCV_core.

R InterPro; IPR005251; HCV_core.

R Pfam; PF01543; HCV_core.
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01-MAR-2004 (TrEMBLrel. 26, Last annotation update) Core, env and part of E2/NS1 (Fragment). Hepatitis C virus.
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Last annotation update)
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Hepatitis C virus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF01560; HCV NS1; 1.
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                                                                                                                                                   NCBI_TaxID=11103;
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                                                                                                                                                                                     1 MSTLPKPQRKTKRNTNRRPTDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRG
                                                                                                                                                                                                          1 MSTLPKPQRKTKRNTNRRPMDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRG
                                                                                                                                                                                                                                                                           61 RROPIPKAROPTGRHWAOPGYPWPLYGNEGCGWAGWLLSPRGSRPNWGPNDPRRRSRNLG
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Pfam; PF01542; HCV core; 1.
Pfam; PF01539; HCV env; 1.
Pfam; PF01560; HCV N31; 1.
Coat protein; Envelpe protein; Glycoprotein; Nonstructural protein;
Polyprotein; Transmembrane.
NON TER 414 414
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Ol-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Core, env and part of E2/NS1 (Fragment).
Hepatitis C virus.
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
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Tokita H., Okamoto H., Luengrojanakul P., Vareesangthip K., Chainuvati T., Iizuka H., Teuda F., Miyakawa Y., Mayumi M.;
"Hepatitis C virus variants from Thailand classifiable into i genotypes in the sixth (6b), seventh (7c,7d) and ninth (9b,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 1011; DB 2; Length 414; Pred. No. 1.1e-76; 0; Mismatches 5; Indels
                                                                                                                          Length 414;
                                                                                                                                                       3; Indels
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                                                                                                                       97.0%; Score 1014; DB 2; 96.9%; Pred. No. 6.1e-77; iive 3; Mismatches 3;
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                                                                                          SEQUENCE 414 AA; 44892 MW;
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Best Local Similarity 97.4
Matches 186; Conservative
                                                                                                                                                       Matches 185; Conservative
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SEQUENCE
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Coat protein; Brwelope protein; Glycoprotein; Nonstructural protein;
POlyprotein; Transmembrane.
NON_TER 414 414
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Hepacivirus.
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0
                                                                                                                                                                                                                                                                              Length 414;
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Okamoto H.;

Submitted (AUG-1996) to the EMBL/GenBank/DDBJ databases.
EMBL, D88472; BAA13621.1; -
EMBL, D88472; BAA13621.1; -
EMBL, C101016021; C:integral to membrane; IEA.

R GO; GO:0015021; C:viral capsid; IEA.

R GO; GO:0019021; C:viral envelope; IEA.

R GO; GO:0019021; C:viral envelope; IEA.

R GO; GO:0019031; C:viral envelope; IEA.

R InterPro; IPR00252; HCV_capsid.

R InterPro; IPR00251; HCV_envelope.

R InterPro; IPR00251; HCV_envelope.

R InterPro; IPR002531; HCV_envelope.
                                                                                                                                                                                                                                                                                                           5; Indels
            GO, GO:0016021; C:integral to membrane, IEA.
GO; GO:0019028; C:viral capsid; IEA.
GO; GO:0019031; C:viral capsid; IEA.
GO; GO:0019031; C:viral envelope; IEA.
GO; GO:0005198; F:seructural molecule activity; IEA.
InterPro; IPR002522; HCV_core.
InterPro; IPR002531; HCV_core.
InterPro; IPR002531; HCV env.
InterPro; IPR002531; HCV env.
Pfam; PF01543; HCV_core; 1.
Pfam; PF01543; HCV_core; 1.
                                                                                                                                                                                                                                               414 AA; 44630 MW; C7DDC84D0198BBD7 CRC64;
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Last annotation update)
                                                                                                                                                                                                                                                                             Score 1016; DB 2;
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96.9%; Pred. No. 4.1e-77;
tive 1; Mismatches 5
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MEDLINE=95062197; PubMed=7972001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
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61 RRQPIPKARQPQGRHWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPHWGPNDPRRRSRNLG 120
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DR GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0016022; C:viral capsid; IEA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019028; C:viral envelope; IEA.
DR GO; GO:0019018; F:structural molecule activity; IEA.
DR GO; GO:00190219; HCV capsid.
DR InterPro; IPR002521; HCV capsid.
DR InterPro; IPR002521; HCV capsid.
DR InterPro; IPR002521; HCV capsid.
DR Ffam; PF01543; HCV capsid.
DR Ffam; PF01543; HCV core; 1.
DR Ffam; PF01544; HCV core; 1.
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Tokita H., Okamoto H., Tsuda F., Song P., Nakata S., Chosa T.,
Tokita H., Mishiro S., Miyakawa Y., Mayuni M.;
Tizuka H., Mishiro S., Miyakawa Y., Mayuni M.;
"Hepatitis C virus variants from Vietnam are classifiable into the seventh, eighth, and ninth major genetic groups.";
Proc. Natl. Acad. Sci. U.S.A. 91:11022-11026(1994).
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Submitted (AUG-1996) to the EMBL/GenBank/DDBJ databases.
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Last annotation update)
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Last annotation update)
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Pred. No. 1.6e-76;
3; Mismatches 4;
                                                                                                                                         414 AA.
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Hepatitis C virus.
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Local Similarity 96.3%;
nes 184; Conservative
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  181 LLSCLTTPASA 191
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and molecular analysis of untypeable samples.";
Wirus Res. 38:137-157(195).

BMBL; L38339; AA0421931.;
GO: GO:0016021; C:integral to membrane; IEA.
GO: GO:0019028; C:viral capsid; IEA.
GO: GO:0019031; C:viral envelope; IEA.
RO: GO:0019198; F:structural molecule activity; IEA.
InterPro: JPR002522; HCV-capsid.
RITERPRO: JPR002519; HCV-capsid.
RITERPRO: JPR002519; HCV-capsid.
RITERPRO: JPR002519; HCV-capsid.
RITERPRO: JPR002519; HCV-capsid.
REPRO: JPR002519; HCV-capsid.
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Stuyver L., Wyseur A., van Arnhem W., Lunel F., Laurent-Puig P., Pawlotsky J.-M., Kleter B., Bassit L., Nkengasong J., van Doorn L.-J., Maertens G.;
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Hepacivirus; Hepatitis C virus type 6.
NCBI_TaxID=31655;
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Hepatitis C virus type 6a.
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MEDLINE=97060095, PubMed=8904416;

A Doi H., Aphichartpiyakul C., Ohba K., Mizokami M., Hotta H.;

A Doi H., Aphichartpiyakul C., Ohba K., Mizokami M., Hotta H.;

Thepatitis C virus (HVV) subtype prevalence in Chiang Mai, Thailand, and identification of novel subtypes of HCV major types 6.";

Li Ciln. Microbiol. 34:569-574(1996).

EMBL; D63946; BAA09976.1;

EMBL; D63946; BAA09976.1;

EMBL; D63946; BAA09976.1;

EMBL; D63946; BAX09376.1;

R GO; GO:0005198; F:structural molecule activity; IEA.

InterPro; IPR002522; HCV_capsid.

R InterPro; IPR002521; HCV_capsid.

R Pfam; PF01542; HCV_core; 1.
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Polyprotein (Fragment).
Hepatitis C virus.
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Hepacivirus.
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Best Local Similarity 95.3%; Pred. No. 1.1e-76;
Matches 182; Conservative 5; Mismatches 4;
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TITLE OF INVENTION: CORE
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                         478139 seqs, 66318000 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries
                                                                                                      protein search, using sw model
                                                                                                                                                                                                                                                                                                                      BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                1 MSTLPKPQRKTKRNTNRRPT.
                                                                                                                                                                                                                                      US-09-084-691B-206
1045
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Maximum DB seq length: 2000000000
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Match Length DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Issued
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93.8
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Perfect score:
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                                                                                                                                                                                                                                                                                Sequence:
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16, App

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18, App
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156,
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NUCLEOTIDE AND DEDUCED
AMINO ACID SEQUENCES OF THE ENVELOPE 1 AND
CORE GENES OF ISOLATES OF HEPATITIS C VIRUS
AND THE USE OF REAGENTS DERIVED FROM THESE
SEQUENCES IN DIAGNOSTIC METHODS AND VACCINES
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Pred. No. 9.3e-97;
US-09-275-265-23
US-09-941-611-23
US-08-290-665A-156
US-08-290-665A-156
US-08-290-665A-159
US-08-290-665A-160
US-08-290-665A-160
US-08-290-665A-160
US-08-290-665A-160
                                                                                                                                                                                                                                                                                                        PCT-US95-10398-156
PCT-US95-10398-157
PCT-US95-10398-159
PCT-US95-10398-169
US-08-635-886C-179
US-08-635-886C-179
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US-08-974-690C-180
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MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPPRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/290,665A
FILING DATE: 15-AUG-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: RIGHARD W. BORK
REGISTRATION NUMBER: 36,459
REFERENCE/DOCKET NUMBER: 2026-4116
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRAX: (212) 751-6849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: BUKH, J., MILLER, R.H. AND APPLICANT: PURCELL, R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 206, Application US/08290665A
Patent No. 5882852
GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 206:
SEQUENCE CHARACTERISTICS:
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Best Local
Matches 19
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                                                            1 MSTLPKPQRKTKRNTNRRPIDVKPPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRG
                                     1 MSTLPKPORKTKRNTNRRPTDVKFPGGGOIVGGVYLLPRRGPRLGVRATRKTSERSOPRG
 Gaps
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APPLICANT: PURCELL, R.H.
TITLE OF INVENTION: WUCLEOTIDE AND DEDUCED
TITLE OF INVENTION: CORE GENES OF ISOLATES OF HEPATITIS C VIRUS
TITLE OF INVENTION: AND THE USE OF REAGENTS DERIVED FROM THESE
TITLE OF INVENTION: AND THE USE OF REAGENTS DERIVED FROM THESE
TITLE OF INVENTION: 2000 SEQUENCES IN DIAGNOSTIC METHODS AND VACCINES
NUMBER OF SEQUENCES: 263
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 0; Indels
 0; Mismatches
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15-AUG-1995
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/086,428
FILING DATE: 29 JUNE 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/290/665
APPLICATION NUMBER: 08/290/665
ATTORNEY/AGENT INFORMATION:
NAME: RICHARD W. BORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MORGAN & FINNEGAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER: 36,459
REFRENCE/DOCKET NUMBER: 20:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
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INDIVIDUAL ISOLATE: HK2
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APPLICATION NUMBER: PCT
FILING DATE: 15-AUG-199
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
 Matches 191; Conservative
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ADDRESSEE: MORGAN & I
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STRANDEDNESS: un
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COUNTRY:
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Length 191;

DB 5;

100.0%; Score 1045;

Query Match

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APPLICANT: LERVOA-NOALS, SELL
APPLICANT: DELEYS, Robert
APPLICANT: DELEYS, Robert
APPLICANT: DELEYS, Robert
TITLE OF INVENTION: IMMUNDOMINANT HUMAN T CELL EPITOPES OF HEPATITIS C
TITLE OF INVENTION: VIRUS
TITLE OF INVENTION: VIRUS
FILE REFERENCE: 2752-18
CURRENT FILING DATE: 1996-04-25
PRIOR APPLICATION NUMBER: DET/EP94/03555
PRIOR APPLICATION NUMBER: BP 93402718.6
PRIOR PAPLING DATE: 1994-10-28
PRIOR PRILING DATE: 1993-11-04
NUMBER OF SEO ID NOS: 286
SOFTWARE: Patentin version 3.1
SEQ ID NO 228
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                              Gaps
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al Similarity 100.0%; Pred. No. 9.3e-97; 191; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-635-886C-228
; Sequence 228, Application US/08635886C
; Patent No. 6555114
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Patent No. 661333
GENERAL INFORMATION:
APPLICANT: LEROUX-ROELS, Geert
APPLICANT: DELEYS, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: LEROUX-ROBLS, Geert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TYPE: PRT
; ORGANISM: hepatitis C virus
US-08-635-886C-228
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61 RRQPIPKARQPEGRSWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPSWGPNDPRRRSRNLG 120
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AMINO ACID SEQUENCES OF THE ENVELOPE 1 AND
CORE GENES OF ISOLATES OF HEPATITIS C VIRUS
AND THE USE OF REAGENTS DERIVED FROM THESE
SEQUENCES IN DIAGNOSTIC METHODS AND VACCINES
                                                                                                                                                                                                                                                                 Length 191;
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Pred. No. 7.3e-92;
4; Mismatches 6;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 15-AUG-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER: 36,459
REFERENCE/DOCKET NUMBER: 2026-4116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 191, Application PC/TUS9510398 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 29 JUNE 1993
PRIOR APPLICATION DATA:
APPLICATION NEWSTRANDED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 08/290/665
FILING DATE: 15 AUGUST 1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: MORGAN & FINNEGAN STREET: 345 PARK AVENUE
                                                        191:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: WORDPERFECT 5.1 CURRENT APPLICATION NUMBER: PCT/US
(212) 758-4800
(212) 751-6849
                                                                                                                                                                                                                                                                       95.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FLOPPY DISK
                                    TELEX: 421792
INPORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
SEGUENCE CHARACTERISTICS:
LENGTH: 191 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           . 345 PARK AVENUE
NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        263
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TITLE OF INVENTION: AMIN
TITLE OF INVENTION: AND
TITLE OF INVENTION: AND
TITLE OF INVENTION: SEQUENCES: 2620
NUMBER OF SEQUENCES: 263
                                                                                                                                                                                              ORGANISM: homosapiens INDIVIDUAL ISOLATE: Z4
                                                                                                                                                                                                                                                                         Query Match 95.3
Best Local Similarity 94.8
Matches 181; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: RICHARD W. BORK
                                                                                                                                   unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          181 LLSCLTTPASA 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LLSCLTVPASA 191
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APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY
                                                                                                                                                        unknown
                                                                                                                   TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NEW YORK
                                                                                                                                                                        ORIGINAL SOURCE:
                                                                                                                                   STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            USA
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                                                                                                                                                          TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
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                      U
                TITLE OF INVENTION:
TITLE OF INVENTION:
VIRUS
CURRENT APPLICATION NUMBER: US/08/974,690C
CURRENT PILING DATE: 1997-11-19
PRIOR APPLICATION NUMBER: PCT/EP94/03555
PRIOR FILING DATE: 1994-10-28
PRIOR FILING DATE: 1993-11-04
NUMBER OF SEQ ID NOS: 286
SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AMINO ACID SEQUENCES OF THE ENVELOPE 1 AND CORE GENES OF ISOLATES OF HERPAITIES C VIRUS AND THE USE OF REAGENIYS DERIVED FROM THESE SEQUENCES IN DIAGNOSTIC METHODS AND VACCINES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/NG-DOS
SOFTWARE: WORDERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/290,665A
FILING DATE: 15-AUG-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 191, Application US/08290665A
Patent No. 5882852
GENERAL INFORMATION:
APPLICANT: BUKH, J., MILLER, R.H. AND
APPLICANT: PURCELL, R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: RICHARD W. BORK
REGISTRATION NUMBER: 36,459
REFERENCE/DOCKET NUMBER: 2026-4116
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: MORGAN & FINNEGAN STREET: 345 PARK AVENUE
                                                                                                                                                                                                                                                                                                  ORGANISM: hepatitis C virus
        MAERTENS, Geert
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TITLE OF INVENTION: AMI
TITLE OF INVENTION: CON
TITLE OF INVENTION: AND
TITLE OF INVENTION: SEQ
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
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NEW YORK
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                                                                                                                                                                                                                                           SEQ ID NO 228
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STATE:
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61 RRQPIPKARRSEGRSWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPSWGPNDPRRRSRNLG 120
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APPLICANT: PURCELL, R.H.
TITLE OF INVENTION: MUCLEOTIDE AND DEDUCED
TITLE OF INVENTION: AMD THE USE OF ISOLATES OF THE ENVELOPE 1 AND
TITLE OF INVENTION: AND THE USE OF REAGENTS DERIVED FROM THESE
TITLE OF INVENTION: SEQUENCES IN DIAGNOSTIC METHODS AND VACCINES
                                                                                                                                                                                                                                                              Length 191;
                                                                                                                                                                                                                                                                                                         7; Indels
                                                                                                                                                                                                                                                         Score 982; DB 2;
Pred. No. 1.8e-90;
5; Mismatches 7
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APPLICATION NUMBER: US/08/290,665A FILING DATE: 15-AUG-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: RICHARD W BORK
REGISTRATION NUMBER: 36,459
REFERENCE/DOCKET NUMBER: 2026-4116
TELECOMMUNICATION:
TELEPHONE: (212) 758-4800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-290-665A-193
; Sequence 193, Application US/08290665A
; Patent No. 5822852
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: MUCLECTIDE AN TITLE OF INVENTION: CORE GENES OF TITLE OF INVENTION: CORE GENES OF TITLE OF INVENTION: SEQUENCES IN NUMBER OF SEQUENCES: 263
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
                                                                                                                                                                                                                                                            94.0%;
93.7%;
                                                LENGTH: 191 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEX: 421792
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 191 amino acids
TYPE: amino acid
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                                                                                                                                                                 ORGANISM: homosapiens INDIVIDUAL ISOLATE: 28
                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 93.7
Matches 179; Conservative
  INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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: NEW YORK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 RROPIPKAROPOGRHWAOPGYPWPLYGNEGCGWAGWLLSPRGSRPHWGPNDPRRRSRNLG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 RRQPIPKARQPEGRSWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPSWGPNDPRRRSRNLG 120
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Patent No. 588282.
GENERAL INFORMATION:
APPLICANT: BUKH, J., MILLER, R.H. AND
APPLICANT: PURCELL, R.H.
TITLE OF INVENTION: NUCLEOTIDE AND DEDUCED
TITLE OF INVENTION: COR GENES OF ISOLATES OF HEPATITIS C VIRUS
TITLE OF INVENTION: AND THE USE OF REAGENTS DERIVED FROM THEISE
TITLE OF INVENTION: AND THE USE OF REAGENTS DERIVED FROM THEISE
TITLE OF INVENTION: ASCOURAGES IN DIAGNOSTIC METHODS AND VACCINES
NUMBER OF SEQUENCES: 263
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Pred. No. 7.3e-92;
4; Migmatches 6; Indels
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REFERENCE/DOCKET NUMBER: 2026-4116
TELECHOMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WORDPERFECT 5.1 CURRENT APPLICATION DATA: US/08/290,665A FILING DATE: 15-AUG-1994
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                                                         TELEX: 421792
INFORMATION FOR SEQ ID NO: 191:
SEQUENCE CHARACTERISTICS:
LENGTH: 191 amino acids
TELECOMMUNICATION INFORMATION:
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IBM PC COMPATIBLE
                                                                                                                                                                                                                                                                                                                                              95.3%;
                     TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 345 PARK AVENUE CITY: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: RICHARD W. BORK
                                                                                                                                    LENGTH: 191 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
                                                                                                                                                                                                                                                  ORGANISM: homosapiens;
INDIVIDUAL ISOLATE: Z4
PCT-US95-10398-191
                                                                                                                                                                                    SS: unknown unknown
                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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181 LLSCLTVPASA 191
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COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY
                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 181; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
                                                                                                                                                                                                       TOPOLOGY: unk
ORIGINAL SOURCE:
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TELEX: 4:
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61 RRQPIPKARRSEGRSWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPSWGPNDPRRRSRNLG 120
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                                                                                                                                                                                                                                                                               1 MSTADRKPORKTKRATANRRPMDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRG 60
                                                                                                                                                                                                                                                1 MSTLPKPORKTKRNTNRRPIDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRG
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NUCLEOTIDE AND DEDUCED
AMINO ACID SEQUENCES OF THE ENVELOPE 1 AND
CORE GENES OF ISOLATES OF HEPATITIS C VIRUS
AND THE USE OF REAGENTS DERIVED FROM THESE
SEQUENCES IN DIAGNOSTIC METHODS AND VACCINES
                                                                                                                                                                                                            .
                                                                                                                                                                  Length 191;
                                                                                                                                                                94.0%; Score 982; DB 5;
93.7%; Pred. No. 1.8e-90;
iive 5; Mismatches 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: BUKH, J., MILLER, R.H. AND APPLICANT: PURCELL, R.H.
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FILING DATE: 15-AUG-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/086,428
FILING DATE: 29 JUNE 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/290/665
FILING DATE: 15 AUGUST 1994
ATTORNEY/AGENT INFORMATION:
NAME: RICHARD W. BORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IEM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: NUCLECTIDE AN TITLE OF INVENTION: AMINO ACID SETTILE OF INVENTION: CORE GENES OF TITLE OF INVENTION: SEQUENCES IN NUMBER OF SEQUENCES: 263
CORRESPONDENCE ADDRESS: ADDRESSER: MORGAN & FINNEGAN STREET: 345 PARK AVENUE CITY: NEW YORK STATE: NEW YORK COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER: 36,459
REFERENCE/DOCKET NUMBER: 20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEX: 421792
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                    Query Match
Best Local Similarity 93.7
Matches 179; Conservative
                                                                                  ORGANISM: homosapiens INDIVIDUAL ISOLATE: Z8
                    SS: unknown unknown
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TYPE: amino acid
STRANDEDNESS: unl
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                                                            ORIGINAL SOURCE:
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                                                                                                                            PCT-US95-10398-192
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                                                                                                                                                                                               Gaps
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ADDRESSEE: MORGAN & FINNEGAN
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                                                                                                                                                  Score 982; DB 2; Length 191;
Pred. No. 1.8e-90;
5; Mismatches 7; Indels
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PCT-UGS9S-10398-192

PCT-UGS9S-10398-192

Sequence 192, Application PC/TUS9510398

GENERAL INFORMATION:
APPLICANT: BUKH, J., MILLER, R.H. AND

ADPLICANT: PURCELL, R.H. AND DEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  UMBER: PCT/US95/10398
15-AUG-1995
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MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION NUMBER: PCT/US95/10396
FILING DATE: 15-AUG-1995
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/086,428
FILING DATE: 29 JUNE 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/290/665
FILING DATE: 15 AUGUST 1994
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REGISTRATION NUMBER: 36,459
REFERENCE/DOCKET NUMBER: 20,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION
                                                                                                                                                       94.0%;
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TELEFAX: (212) 751-6849
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                     Query Match
Best Local Similarity 93.7
Matches 179; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: RICHARD W. BORK
                          TOPOLOGY: unknown
ORIGINAL SOURCE:
ORGANISM: homosapiens
INDIVIDUAL ISOLATE: Z1
      unknown
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NEW YORK
      STRANDEDNESS:
                                                                                                             US-08-290-665A-193
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61 RROPIPKAROPOGRHWAOPGYPWPLYGNEGCGWAGWLLSPRGSRPHWGPNDPRRRSRNLG 120
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                                                                                                                                                                                                                                1 MSTNPKPQRKTKRNTNRRPQDVKFPGGGQIVGCVYLLPRRGPRLGVRATRKTSERSQPRG 60
                                                                                                                                                                                                                                                                                                              61 RRQPIPKARQPEGRITWAQPGYPWPLYGNEGMGWAGWLLSPRGSRPNWGPTDPRRRSRNLG
                                                                                                                                                                                                1 MSTLPKPQRKTKRNTNRRPTDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRG
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APPLICANT: PURCELL, R.H.
TITLE OF INVENTION: MINO ACID SEQUENCES OF THE ENVELOPE 1 AND
TITLE OF INVENTION: CORE SERIES OF PREPAITIES C VIRUS
TITLE OF INVENTION: CORE SERIES OF REAGENTS OF HERPAITIES C VIRUS
TITLE OF INVENTION: SEQUENCES IN DIAGNOSTIC METHODS AND VACCINES
                                                                                                             Length 191;
                                                                                                         93.9%; Score 981; DB 2; Length 19
93.7%; Pred. No. 2.3e-90;
ive 5; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: PCT/US95/10398
PILING DATE: 15-AUG-1995
CLASSIPTCATION:
PLOR APPLICATION DATA:
APPLICATION NUMBER: 08/086,428
FILING DATE: 29 JUNE 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/086,428
FILING DATE: 15 AUGUST 1994
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 172, Application PC/TUS9510398 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WORDPERFECT 5.1 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: MUCLEOTIDE AS ITTLE OF INVENTION: AMINO ACID SI TITLE OF INVENTION: CORE GENES OF TITLE OF INVENTION: SEQUENCES IN NUMBER OF SEQUENCES: 263
CORRESPONDENCE ADDRESS: ADDRESSE: ADDRESSE: ADDRESSE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: RICHTARD W. BORK
REGISTRATION NUMBER: 36,459
REFERENCE/DOCKET NUMBER: 2026
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLUM TYPE: FLOPPY DISK COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MC
                      RGANISM: homosapiens
NDIVIDUAL ISOLATE: HK3
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TYPE: amino acid
                                                                                                                               Best Local Similarity 93.7
Matches 179; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEX: 421792
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY
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    ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino a STRANDEDNESS:
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US-08-290-665A-172
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                          ORGANISM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET:
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                                                                                                             Query Match
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                                                                                                                                                                                                                                                                                                                                                                61 RROPIPKAROPOGRHWAOPGYPWPLYGNEGCGWAGWLLSPRGSRPHWGPNDPRRRSRNLG
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APPLICANT: BUKH, J., R.H.
APPLICANT: BURCELL, R.H.
TITLE OF INVENTION: NUCLECTIDE AND DEDUCED
TITLE OF INVENTION: CORE GENES OF ISOLATES OF HEPATITIS C VIRUS
TITLE OF INVENTION: AND THE USE OF REAGENTS DERIVED FROM THESE
TITLE OF INVENTION: SEQUENCES IN DIAGNOSTIC METHODS AND VACCINES
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                       ;
                                                                                                                                                                                              Length 191;
                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                            Score 982; DB 5;
Pred. No. 1.8e-90;
                                                                                                                                                                                                                                  5; Mismatches
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ZIP: 10.154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC CONTATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDERFECT 5.1
CURRENT APPLICATION DATA:
FILING DATE: 15-AUG-1994
CLASSIFICATION TOWBER: US/08/290,655A
FILING DATE: 15-AUG-1994
CLASSIFICATION WHERE: 36,459
REGISTRATION W. BORR
REGISTRATION NUMBER: 36,459
REGISTRATION NUMBER: 36,459
REPERENCE/DOCKET NUMBER: 30,459
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-290-665A-172; Sequence 172, Application US/08290665A; Patent No. 582852; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEX: 421792
INFORMATION FOR SEQ ID NO: 172:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                       Query Match
Best Local Similarity 93.7%;
Matches 179; Conservative
191 amino acids
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                                                                                JANUARISM: DOMOSAPIENS ; INDIVIDUAL ISOLATE: Z1 PCT-US95-10398-193
                                        unknown
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                 TYPE: amino acid
STRANDEDNESS: unkn
TOPOLOGY: unknown
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STRANDEDNESS: unkr
TOPOLOGY: unknown
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NEW YORK
                                                                              ORIGINAL SOURCE:
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STREET: 34
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STATE:
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61 RRQPIPKARQPQGRHWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPHWGPNDPRRRSRNLG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                  KVIDTLTCGFADLMGYIPVVGAPLGGVAAALAHGVRAIEDGINYATGNLPGCSFSIFLLA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MSTLPKPORKTKRNTNRRPTDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N.H.
NUCLECTIDE AND DEDUCED
AMINO ACID SEQUENCES OF THE ENVELOPE 1 AND
CORR GENES OF ISOLATES OF HEPATITIS C VIRUS
AND THE USE OF REAGENTS DERIVED FROM THESE
SEQUENCES IN DIAGNOSTIC METHODS AND VACCINES
                                                        Length 191;
                                                        93.8%; Score 980; DB 2; 93.7%; Pred. No. 2.9e-90;
                                                                                                                   4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: BUKH, J., MILLER, R.H. AND APPLICANT: PURCELL, R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 15-AUG-1995
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 197, Application PC/TUS9510398 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERECT 5.1
CURRENT APPLICATION DRATA:
APPLICATION NUMBER: PCT/US95/10396
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APPLICATION DATA:
APPLICATION NUMBER: 08/086,428
FILING DATE: 29 JUME 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/290/665
FILING DATE: 15 AUGUST 1994
ATTORNEY/AGENT INFORMATION:
NAME: RICHARD W. BORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: PURCELL, R.H.
TITLE OF INVENTION: NUCLEOTIDE AN
TITLE OF INVENTION: AMINO ACID SE
TITLE OF INVENTION: CORE GENES OF
TITLE OF INVENTION: AND THE USE OF
TITLE OF INVENTION: SEQUENCES IN
NUMBER OF SEQUENCES: 263
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER: 36,459
REFERENCE/DOCKET NUMBER: 205
TELECOMMUNICATION INFORMATION:
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INFORMATION FOR SEQ ID NO: 197:
SEQUENCE CHARACTERISTICS:
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CITY: NEW YORK
STATE: NEW YORK
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                                                     Query Match
Best Local Similarity 93.7
Matches 179; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LLSCLTTPASA 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181 LLSCLTVPASA 191
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US-08-290-665A-197
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Pred. No. 2.3e-90;
5; Mismatches 7; Indels
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COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDERRECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/290,665A
FILING DATE: 15-AUG-1994
ATHORNEV/ACTIVE
ATHORNEV/AC
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NAME: RICHARD W. BORK
REGISTRATION NUMBER: 36,459
REPRENCE/DOCKET NUMBER: 2026-4116
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MILLER, R.H. AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 197, Application US/08290665A; Patent No. 5882852
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INFORMATION FOR SEQ ID NO: 197:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                              93.9%;
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INDIVIDUAL ISOLATE: DK13
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TYPE: amino acid
                            INDIVIDUAL ISOLATE: HK3 PCT-US95-10398-172
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: NUCL.
TITLE OF INVENTION: AMINITITLE OF INVENTION: CORE TITLE OF INVENTION: AND NUMBER OF SEQUENCES: 263 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                         Matches 179; Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY I
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      TOPOLOGY: unknown
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Best Local Similarity
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NEW YORK
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Baten No. 6555114

GENERAL INFORMATION:
APPLICANT: LEROUX-ROELS, Geert
APPLICANT: DELEYS, Robert
APPLICANT: DELEYS, Robert
TITLE OF INVENTION: URWOOD INVENTION: URWOOD INVENTION: URWER;
FILE REFERENCE: 2752-18
CURRENT APPLICATION NUMBER: US/08/635,886C
CURRENT FILING DATE: 1996-04-25
PRIOR APPLICATION NUMBER: EP94/03555
PRIOR PELLING DATE: 1994-10-28
PRIOR PELLING DATE: 1994-10-28
PRIOR PELLING DATE: 1993-11-04
NUMBER OF SEQ ID NOS: 286
SOFTWARE: Patentin Version 3.1
SEQ ID NOS: 286
SEQ ID NOS: 286
SEQ ID NOS: 286
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                                                      Length 191;
                                                                                      8; Indels
                                                Score 980; DB 5;
Pred. No. 2.9e-90;
4; Mismatches 8;
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                                                  Query Match 93.8%;
Best Local Similarity 93.7%;
Matches 179; Conservative
INDIVIDUAL ISOLATE: DK13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: hepatitis C virus
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Matches 179; Conservative
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PCT-US95-10398-197
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US-08-635-886C-217
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| cgn2 6/ptodata1/lpubpaa/US07 PUBCOMB.ppp:*
| cgn2 6/ptodata1/lpubpaa/US07 NEW PUB.ppp:*
| cgn2 6/ptodata1/lpubpaa/US06 NEW PUB.ppp:*
| cgn2 6/ptodata1/lpubpaa/US06 PUBCOMB.ppp:*
| cgn2 6/ptodata1/lpubpaa/US07 NEW PUB.ppp:*
| cgn2 6/ptodata1/lpubpaa/PCTUS PUBCOMB.ppp:*
| cgn2 6/ptodata1/lpubpaa/US08 NEW PUB.ppp:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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Sequence 229, App Sequence 181, App Sequence 23, Appl Sequence 24, Appl Sequence 179, App Sequence 180, App Sequence 56, Appl Sequence 4, Appli Sequence 9, Appli Sequence 228, App Sequence 217, App Sequence 42, Appl Description S US-10-651-165-229 S US-10-651-165-181 US-09-941-611-23 4 US-10-044-995-23 5 US-10-365-620-54 5 US-10-365-620-56 5 US-10-365-620-56 5 US-10-365-620-56 5 US-10-365-620-56 US-10-651-165-228 US-10-651-165-217 US-09-851-138-42 Query Match Length DB 0.000 000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.

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Sequence 1, Appli Sequence 20, Appl Sequence 3, Appli Sequence 1, Appli Sequence 2, Appli Sequence 2, Appli	اِس بِا عِمِ بِا ''در	Sequence 2, Appli Sequence 20, Appli Sequence 20, Appl Sequence 20, Appl Sequence 20, Appl	equence 189 equence 2, 8 equence 2, 8 equence 2, 8 equence 3, 8 equence 3, equence 3, equence 18	11427000
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ALIGNMENTS

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GENERAL INVENDATION:
APPLICANT: LEROUT-ROBLS, Geert
APPLICANT: DELEYS, Robert
APPLICANT: DELEYS, Robert
APPLICANT: MARKTENS, Geert
TITLE OF INVENTION: IMMUNDCOMINANT HUMAN T CELL EPITOPES OF HEPATITIS C
TITLE OF INVENTION: IMMUNDCOMINANT HUMAN T CELL EPITOPES OF HEPATITIS C
TITLE OF INVENTION: VARUS
FILE REFERENCE: 2551-94
CURRENT FILING DATE: 2003-09-02
PRIOR PILING DATE: 1997-11-19
PRIOR PLICATION NUMBER: PCT/EP94/03555
PRIOR APPLICATION NUMBER: PCT/EP94/03555
PRIOR PLING DATE: 1994-10-28
PRIOR PLING DATE: 1994-10-28
PRIOR PLING DATE: 1993-11-04
NUMBER OF SEQ ID NOS: 286
SOFTWARE: PatentIn version 3.1
SEQ ID NO 228
LENGTH AND
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Best Local Similarity 100.0%; Pred. No. 1.1e-83;
Matches 191; Conservative 0; Mismatches 0; Indels 0;
              Sequence 228, Application US/10651165
Publication No. US20040047877A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: hepatitis C virus US-10-651-165-228
US-10-651-165-228
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APPLICANT: DELEYS, ROBERT
APPLICANT: DELEYS, ROBERT
APPLICANT: MARRIENS, Geert
TITLE OF INVENTION: IMMONODOMINANT HUMAN T CELL EPITOPES OF HEPATITIS C
TITLE OF INVENTION: VIRUS
FILE OF INVENTION: VIRUS
FILE OF DATE: 2551-94
CURRENT APPLICATION NUMBER: US/10/651,165
CURRENT APPLICANTON NUMBER: US/08/974,690C
PRIOR FILING DATE: 1997-11-19
PRIOR FILING DATE: 1997-11-19
PRIOR FILING DATE: 1994-10-28
PRIOR FILING DATE: 1994-10-28
PRIOR FILING DATE: 1993-11-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MSTLPRPQRKTKRNTNRRPMDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 RRQPIPKVRQPTGRSWGQPGYPWPLYGNBGCGWAGWLSPRGSRPNWGPNDPRRRSRNLG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 319;
                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Microsoft Word 6.0 / ASCII text output
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/851,138
FILING DATE: 09-May-2001
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 977; DB 9; L. Pred. No. 1.1e-77; 3; Mismatches 9;
                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 08/836,075
FILING DATE: «UDKNOWN)
APPLICATION NUMBER: EP 94870166.9
FILING DATE: 21 OCT 1994
APPLICATION NUMBER: EP 95870076.7
FILING DATE: 28 UN 1 1995
ATTORNY AGENT INFORMATION:
NAME: KAMMERER, PATRICIA A.
REGISTRATION NUMBER: 29,775
REGISTRATION NUMBER: 29,775
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 42:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 229, Application US/10651165
Publication No. US20040047871781
GENERAL INFORMATION:
APPLICANT: LEROUX-ROELS, Geert
                                                            COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 319 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  93.5%;
93.7%;
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Best Local Similarity 93.7
Matches 179; Conservative
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61 RRQPIPKARQLEGRSWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPSWGPNDFRRRSRNLG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 KVIDTLICGFADIMGYIPVVGAPLGGVAAALAHGVRAIEDGINYATGNLPGCSFSIFLLA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 RRQPIPKARQPQGRHWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPHWGPNDPRRRSRNLG 120
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                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: DELEYS, Robert
APPLICANT: DELEYS, Robert
APPLICANT: DELEYS, Robert
TITLE OF INVENTION: IMMUNODOMINANT HUMAN T CELL EPITOPES OF HEPATITIS C
TITLE OF INVENTION: VIRUS
FILE REPRENCE: 2551-94
CURRENT APPLICATION NUMBER: US/10/651,165
CURRENT PILING DATE: 1997-11-19
PRIOR FILING DATE: 1997-11-19
PRIOR FILING DATE: 1994-10-28
PRIOR FILING DATE: 1993-11-04
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Pred. No. 5.9e-78;
4; Mismatches 8;
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CORRESPONDENCE ADDRESS:
ADDRESSEE: ARNOLD, WHITE & DURKEE
                                                                                                                                                                                                                                                                                         Sequence 217, Application US/10651165
Publication No. US20040047877A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 42, Application US/09851138 Publication No. US20020183508A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: MAERTENS, GEERT
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Best Local Similarity 93.7%;
Matches 179; Conservative
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SEQ ID NO 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TYPE: PRT
; ORGANISM: hepatitis C virus
US-10-651-165-217
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LLSCLTVPASA 191
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US-10-651-165-217
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US-09-851-138-42
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61 RRÓPIPKVRRPEGRIWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPSWGPTDPRRRSRNLG 120
1 MSTIPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVXLLPRRGPRLGVRATRKTSERSQPRG 60
                                                                                                                                               KVIDTLICGFADLMGYIPVVGAPLGGVAAALAHGVRAIBDGINYATGNLPGCSFSIFLLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ANTIGENS FOR THE DETECTION OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 977; DB 9; Length 2894; Pred. No. 1.2e-76; 6; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: DATEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/941,611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MAERIENS, GEERT
VAN HEUVERSWUN, HUGO
TITLE OF INVENTION: SYNTHEFIC ANTIGENS FOR THE DETER
ANTIBODIES TO HEPATITIS C VIRUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 30-Aug-2001
CLIASSIPICATION
PRIOR APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 1995-02-21
FILING DATE: 1955-02-21
FILING DATE: 1955-02-21
FILING DATE: 13-DEC-1991
APPLICATION NUMBER: WO PT/EP91/02409
FILING DATE: 13-DEC-1990
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 1487-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; SEQUENCE DESCRIPTION: SEQ ID NO: 23:
US-09-941-611-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: SADOFF, B.J.
REGISTRATION NUMBER: 36,663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION: TELEPHONE: 7038164000
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SEQUENCE CHARACTERISTICS:
LENGTH: 2894 amino acids
                                                                                                                                                                                                                                                                                                                                                                      Sequence 23, Application US/09941611 Patent No. US20020106640A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: DELEYS, ROBERT J
POLLET, DIRK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 93.5%;
Best Local Similarity 92.1%;
Matches 176; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: ARLINGTON STATE: VA
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                                                                                                                                                                                                                                                                                                                                                     US-09-941-611-23
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Publication No. US20040047877A1

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
CENERAL INFORMATION:
TITLE OF INVENTION: IMMUNODMINANT HUMAN T CELL EPITOPES OF HEPATITIS C
TITLE OF INVENTION: IMMUNODMINANT HUMAN T CELL EPITOPES OF HEPATITIS C
TITLE OF INVENTION: IMMUNODMINANT HUMAN T CELL EPITOPES OF HEPATITIS C
TITLE OF INVENTION: VIRUS
FILE REPERENCE: 2551-94
CURRENT APPLICATION NUMBER: US/08/974,690C
FRICK FILING DATE: 1997-11-19
FRIOR FILING DATE: 1997-11-02
FRIOR FILING DATE: 1994-10-28
FRIOR FILING DATE: 1994-10-28
FRIOR FILING DATE: 1993-11-04
NUMBER OF SEQ ID NOS: 286
SEQ ID NOS: 286
SEQ ID NO 181
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                                                                                                                                                                                                                                                                                                                                                                                                                Score 977; DB 15;
Pred. No. 1.1e-77;
3; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 977; DB 15;
Pred. No. 1.6e-77;
6; Mismatches 9;
                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: Xaa is any amino acid US-10-651-165-229
                                                                                                                                                                                               any amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    93.5%;
92.1%;
                                                                                                                                                                                                                                 NAME/KEY: MISC FEATURE
LOCATION: (308)...(308)
OTHER INFORMATION: Xaa is any
                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 93.5%;
Best Local Similarity 93.7%;
                                 PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT ORGANISM: hepatitis C virus
                                                                                                             ORGANISM: hepatitis C virus FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 176; Conservative
                                                                                                                                                                    LOCATION: (128)...(129)
OTHER INFORMATION: Xaa is
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 179; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LLSCLTTPASA 191
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            NUMBER OF SEQ ID NOS: 286
                                                                                                                                                                                                                                                                                              FEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (310)...(310)
                                                                                                                                                       NAME/KEY: MISC_FEATURE
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Best Local Similarity
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                               SOFTWARE: Pate
SEQ ID NO 229
LENGTH: 319
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61 RRQPIPKARQPQGRHWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPHWGPNDPRRRSRNLG 120
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                                                                                                                1 MSTIPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRG 60
                                                                                                                                                                                                                                                                                  121 KVIDTLICGFADLMGYIPLVGAPLGGAARALAHGVRVLEDGVNYATGNLPGCSFSIFLLA
                                                                                       1 MSTLPKPQRKTKRNTNRRPTDVKFPGGGOIVGGVYLLPRRGPRLGVRATRKTSERSOPRG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   91 RRQPIPKARRPEGRTWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPSWGPTDPRRRSRNLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: George, Rajan
APPLICANT: Tyrrell, Lorne
APPLICANT: Tyrrell, Lorne
APPLICANT: Tyrrell, Lorne
APPLICANT: Wo. US20040001853Aljaim, Antoine
TITLE OF INVENTION: Chimeric Antigens for Eliciting An Immune Response
FILE REFERENCE: 656.0016
CURRENT FILING DATE: 2003-02-13
FRIOR APPLICATION NUMBER: US6/423,578
FRIOR APPLICATION NUMBER: G0/390,564
                                                Gaps
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  Length 2894;
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  Score 977; DB 14;
Pred. No. 1.2e-76;
6; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         93.4%; Score 976; DB 15; 92.7%; Pred. No. 1e-77;
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5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequence 179, Application US/10651165; Publication No. US20040047877A1
EDBLICATION NO. USCOME SENERAL INFORMATION:
APPLICANT: LEROUX-ROELS, Geert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 54, Application US/10365620
; Publication No. US20040001853A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: PRT
; ORGANISM: ORF of HCV Core Protein
US-10-365-620-54
    93.5%;
92.1%;
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NUMBER OF SEQ ID NOS: 76
SOFTWARE: Patentin version 3.2
SEQ ID NO 54
Query Match
Best Local Similarity 92.13
Matches 176; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 92.7
Matches 177; Conservative
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|LLSCLTVPASA 191
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                                                                                   RROPIPKAROPOGRHWAOPGYPWPLYGNEGCGWAGWLLSPRGSRPHWGPNDPRRRSRNLG 120
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                          1 MSTIPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPPRRGPRLGVRATRKTSERSQPRG
                                                                                                                                                                                             MSTLPKPQRKTKRNTNRRPTDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MAERTENS, GEERT
VAN HEUVERSWUN, HUGO
TITLE OF INVENTION: SYNTHETIC ANTIGENS FOR THE DETECTION OF
ANTIBODIES TO HEPATITIS C VIRUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC_compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: 08/391,671
FILING DATE: -Unknown>
FILING DATE: -Unknown>
FILING DATE: 14-0CT-1992
APPLICATION NUMBER: WO PCT/EP91/02409
FILING DATE: 13-DEC-1991
APPLICATION NUMBER: EP 90124241.2
FILING DATE: 14-DEC-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/044,995
FILING DATE: 15-Jan-2002
CLASSIFICATION: <UNKnown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ANTI-SENSE: NO
SEQUENCE DESCRIPTION: SEQ ID NO: 23:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: SADOFF, B.J.
REGISTRATION NUMBER: 36,663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 7038164000
                                                                                                                                                                                                                                                                                                                                                             RESUL: ,
US-10-044-995-23
US-10-044-995-23; Application US/10044995
; Publication No. US20030049685A1
; GENERAL INFORMATION:
APPLICANT: DELEYS, ROBERT J
POLICANT: POLLET, DIRK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 2894 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
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COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                        LLSCLTTPASA 191
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RRQPIPKARQPQGRHWAQPGYFWPLYGNECGWAGWLLSPRGSRPHWGPNDPRRSRNLG 120
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                      Query Match 93.4%; Score 976; DB 15; Length 473; Best Local Similarity 92.7%; Pred. No. 2e-77; Matches 177; Conservative 5; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: PRT
; ORGANISM: ORF of HCV Core-TBD protein
US-10-365-620-56
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Ingravallo, Paul
Wright-Minogue, Jacquelyn
Lau, Johnson Y.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hong, Zhi
Butkiewicz, Nancy J.
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; Sequence 180, Application US/204047877A1
; GENERAL INFORMATION:
; APPLICANT: LEROUX-ROELS, Geert
; APPLICANT: LEROUX-ROELS, Geert
; APPLICANT: DELENOX-ROELS, Geert
; TITLE OF INVENTION: INMUNDOMINANT HUMAN T CELL EPITOPES OF HEPATITIS C
; TITLE OF INVENTION: VIRUS
; FILE REFERENCE: 2551-94
; CURRENT APPLICATION NUMBER: US/08/974,690C
; FILE REPERENCE: 1997-11-19
; PRIOR PILING DATE: 1997-11-19
; PRIOR PILING DATE: 1997-11-06
; PRIOR PILING DATE: 1997-11-07
; PRIOR FILING DATE: 1997-11-07
; RUGHER APPLICATION NUMBER: EP 93402718.6
; PRIOR FILING DATE: 1993-11-04
; NUMBER OF SEQ ID NOS: 286
; SOFTWARE: PATENTIN VOISION 3.1
; SEQ ID NO 180
; LENGTH: 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 RRQPIPKARQPQGRHWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPHWGPNDPRRRSRNLG 120
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APPLICANT: DELEYS, Robert
APPLICANT: MARRTENS, Geert
TITLE OF INVENTION: IMMUNDOMINANT HUMAN T CELL EPITOPES OF HEPATITIS C
TITLE OF INVENTION: VINUS
FILE REFERENCE: 2551-94
CURRENT PELLONION NUMBER: US/10/651,165
CURRENT PELLONION NUMBER: US/08/974,690C
PRIOR PELLONION NUMBER: US/08/974,690C
PRIOR FILING DATE: 1997-11-19
PRIOR FILING DATE: 1994-10-28
PRIOR FILING DATE: 1994-10-28
PRIOR FILING DATE: 1994-10-28
PRIOR FILING DATE: 1994-10-28
PRIOR PLICATION NUMBER: EP 93402718.6
PRIOR FILING DATE: 1993-11-04
NUMBER OF SEQ ID NOS: 286
SOFTWARE: PATENTIN VERSION 3.1
SEQ ID NO 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MSTNPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRG
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93.4%; Score 976; DB 15; Length 450;
Best Local Similarity 92.7%; Pred. No. 1.9e-77;
Matches 177; Conservative 5; Mismatches 9; Indels C
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Pred. No. 1.9e-77;
5; Mismatches 9;
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Best Local Similarity 92.7%;
Matches 177; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TYPE: PRT
; ORGANISM: hepatitis C virus
US-10-651-165-179
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US-10-651-165-180
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ORGANISM: Artificial Sequence
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US-09-929-955-1
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LENGTH: 3011
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Patent No. US20020119495A1
GENERAL INFORMATION:
APPLICANT: HAWAII BIOTECHNOLOGY GROUP, Inc.
APPLICANT: NAKANO, Eileen
TITLE OF INVENTION: IMMUNOGENIC COMPOSITION OF HEPATITIS C
FILE REFERENCE: HAWBIOLIO
CURRENT APPLICATION NUMBER: US/09/952,572
CURRENT APPLICATION NUMBER: US/09/952,572
PRIOR PRILING DATE: 2001-09-13
PRIOR PLING DATE: 2000-09-13
PRIOR FILING DATE: 2000-09-13
PRIOR FILING DATE: 2000-09-13
                                                                                                                                                                                                                                                                              Score 976; DB 9; Length 3011;
Pred. No. 1.5e-76;
5; Mismatches 9; Indels
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Pred. No. 1.5e-76;
5; Mismatches 9; Indels
APPLICANT: Lemon, Stanley M.
TITLE OF INVENTION: Chimeric HCV/GBV-B viruses
FILE REFERENCE: 1D01116
CURRENT APPLICATION NUMBER: US/09/742,659
PRIOR APPLICATION NUMBER: US 60/171,469
PRIOR FILING DATE: 1999-12-22
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 93.4%;
Best Local Similarity 92.7%;
Matches 177; Conservative E
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Best Local Similarity 92.7%;
Matches 177; Conservative
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                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Hepatitis C virus
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Best Local Similarity
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LENGTH: 3011
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APPLICANT: Lemon, Stanley
APPLICANT: Lemon, Stanley
APPLICANT: Ti MinKyung
TITLE OF INVENTION: REPLICATION COMPETENT HEPATITIS C VIRUS AND METHODS OF USE
FILE REPERBNCE: 265.0007 0101
CURRENT PILING DATE: 2000-12-23
PRIOR APPLICATION NUMBER: US 60/171,909
PRIOR FILING DATE: 1999-12-23
NUMBER OF SEQ ID NOS: 34
SOCTWARER PATENTION OF USED IN OS: 34
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121 KVIDTLTCGFADLMGYIPLVGAPLGGAARALAHGVRVLEDGVNYATGNLPGCSFSIFLLA 180
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93.4%; Score 976; DB 9; Length 30
Best Local Similarity 92.7%; Pred. No. 1.5e-76;
Matches 177; Conservative 5; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                          Sequence 1, Application US/09929955
Patent No. US20020136740A1
GENERAL INPORMATION:
APPLICANT: Matti Sallberg
APPLICANT: Catharina Hultgren
TITLE OF INVENTION: WACTORES CONTAINING RIBAVIRIN AND
TITLE OF INVENTION: WACTORES CONTAINING RIBAVIRIN AND
TITLE OF INVENTION: WACTORES CONTAINING RIBAVIRIN AND
TITLE REFERENCE: TRIPEP 23AUS2
CURRENT APPLICATION NUMBER: US/09/929,955
CURRENT FILING DATE: 2000-08-15
PRIOR APPLICATION NUMBER: 09/705,547
PRIOR APPLICATION NUMBER: 60/229,175
PRIOR APPLICATION NUMBER: 1000-08-17
NUMBER OF SEC ID NOS: 49
SEC ID NO 1
LINGURH 13011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; OTHER INFORMATION: Hepatitis C virus sequence
US-09-929-955-1
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Patent No. US20020155582A1
GENERAL INFORMATION:
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Search completed: October 30, 2004, 01:49:51 Job time : 130 secs

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Hepatitis
Hepatitis
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Aar66633 Hepatitis
Aaw30597 Hepatitis
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Adr668080
Adr29529
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Adr92995
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Aar34472
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GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                          2002273 seqs, 358729299 residues
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                                protein search, using sw model
                                                October 30, 2004, 01:46:14
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Aar34478 Encoded b	Aar34474 Encoded b	Aar34477 Encoded b	Aar34476 Encoded b	Aar34479 Encoded b	Aar34473 Encoded b	Aar34475 Encoded b	Aar34469 Encoded b	Aar34467 Encoded b		Aam47263 Cuticle p	Aam47265 Cuticle p	Adj82984 Adenovect	Aar54067 Non-A, no	Aar98362 5'UTR/COR	Abg32458 Hepatitis				
AAR34478	AAR34474	AAR34477	AAR34476	AAR34479	AAR34473	AAR34475	AAR34469	AAR34467	AAR34471	AAM47263	AAM47265	ADJ82984	AAR54067	AAR98362	ABG32458	ABG32459	ABG32451	ABG32455	ABG32457
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51	21	51	21	51	21	21	21	51	21	21	51	21	21	51	21	21	51	51	21
26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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DNA and amino acid sequence of HCV envelope 1 and core proteins - used to determine HCV genotype and as vaccines against HCV infection.
                                                                       1; core protein; HCV genotyping; antibody; vaccine;
                                                        core protein.
       AAR92987 standard; protein; 191 AA
                                                                                                                                                                                                                                                               Claim 4; Page 223; 340pp; English
                                                                                                                                                                                                Purcell RH;
                                                       Hepatitis C virus isolate HK2
                                                                                                                                               95WO-US010398.
                                                                                                                                                                94US-00290665
                                                                                                                                                                                (USSH ) US SEC DEPT HEALTH
                                      (first entry)
                                                                                                                                                                                                                WPI; 1996-139709/14.
N-PSDB; AAT16661.
                                                                                                                                                                                                Bukh J, Miller RH,
                                                                        envelope
                                                                                                Hepatitis C virus.
                                                                                                               WO9605315-A2.
                                                                                                                                               15-AUG-1995;
                                                                                                                                                                15-AUG-1994;
                                       02-OCT-1996
                                                                                                                                22-FEB-1996.
                                                                               hepatitis.
                       AAR92987;
AAR92987
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AAR92936-R92987 are HCV core proteins derived from 52 different HCV isolates. Isolated cDNA sequences are used for the prodn. of primers useful for detecting the presence of HCV in a sample, the primers are also useful for HCV genotyping. Proteins encoded by the cDNAs can be used in vaccines for immunising against HCV infection. The proteins may also be used to detect antibodies against HCV in serum, saliva, lymphocytes or other monomuclear cells. The antibodies may be used in the prevention of

Score 191; DB 2; Length 191; Pred. No. 1.9e-167;

100.0%; 100.0%;

Query Match Best Local Similarity

Sequence 191 AA; HCV infection

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N-PSDB; AAX00458
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24-FEB-1994;
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                                                                                                                                                                                       05-JAN-1999
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                                                                       AAW30597;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
           21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local
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Matches
                                              AAW30597
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                                                                       120
                                                                                                   61 RRQPIPKARQPGGRHWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPHWGPNDPRRRSRNLG 120
                                                                                        KVIDTLICGFADLMGYIPVVGAPLGGVAAALAHGVRAIEDGINYATGNLPGCSFSIFLLA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAQ79776 encodes AAR66633 the prod. of the hepatitis C virus (HCV) J1 core domain consensus sequence. They can be used to provide new oligonucleotides and polypeptides for use in diagnostics, recombinant protein prodn. and anti-HCV vaccine development. (Updated on 25-MAR-2003 to correct PF field.)
                     9
                                     9
                                                                 1 MSTLPKPQRKTKRNTNRRPTDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRG
                                1 MSTLPKPQRKTKRNTNRRPTDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Method of detecting hepatitis C virus polynucleotide - utilises probe based on DNA of new HCV isolates J1 and J7.
    Gaps
                                                                                                                                                                                                                                                                    Hepatitis C virus J1 core domain; anti-HCV vaccine development; non-A non-B virus; diagnostic polypeptides; HCV probes.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Houghton M;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ch 26.7%; Score 51; DB 2; Length 97; 1 Similarity 100.0%; Pred. No. 8e-39; 51; Conservative 0; Mismatches 0; Indels
    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                         Kolberg JA,
                                                                                                                                                                                                                                                     Hepatitis C virus J1 core domain consensus protein.
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    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                         Saito I, Miyamura T, Cha T,
3D, Weiner AJ;
                                                                                                                                                                                        AAR66633 standard; protein; 97 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                CHIRON CORP.

NAT INST OF HEALTH JAPAN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Fig 18; 45pp; English
                                                                                                                                                                                                                                                                                                                                                                  89US-00408045.
89US-00456142.
91US-00637380.
93US-00101280.
                                                                                                                                                                                                                                                                                                                                                    94US-00201066.
                                                                                                                                                                                                                            (revised)
(first entry)
    Matches 191; Conservative
                                                                                                                             LLSCLTTPASA 191
                                                                                                                                        LLSCLTTPASA 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1995-030306/04.
                                                                                                                                                                                                                                                                                                Hepatitis C virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; AAQ79776
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 97 AA;
                                                                                                                                                                                                                                                                                                                                                                            21-DEC-1989;
04-JAN-1991;
02-AUG-1993;
                                                                                                                                                                                                                                                                                                                                                   24-FEB-1994;
                                                                                                                                                                                                                                                                                                                                                                    15-SEP-1989;
                                                                                                                                                                                                                           25-MAR-2003
31-AUG-1995
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Irvine BD,
                                                                                                                                                                                                          AAR66633;
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This polypeptide comprises a core protein of novel Japanese isolate J1 of hepatitis C virus (HCV), as deduced from an amplified DNA clone (see AAX00458). The sequence shows homology to prototype HCV-1. The invention provides new Japanese isolates, J1 and J7, of HCV. The new isolates have nucleotide and amino acid sequences which are distinct from the prototype HCV-1 isolate. These differences can be exploited for use in diagnostics (for NANDH, recombinant protein production and vaccine development.

Claimed antigenic polypeptides (see AAM30583-87) can be used: (i) as immunoassay reagents, or standards, to detect HCV antibodies, e.g. for diagnosing infection or screening donated blood; (ii) to generate specific antibodies (used for detecting the corresponding polypeptide, to screen for antiviral agents, for virus isolation and for passive immunisation); (iii) in protective or therapeutic vaccines, and (iv) for isolation of non-A, non-B viruses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              - useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Saito I;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Antigenic polypeptides from J1 and J7 hepatitis C virus isolates as immunoassay reagents, for raising antibodies and as vaccine
                                                                                                                                                                                                                  HCV; non-A, non-B hepatitis; NANBH; diagnosis; vaccine; antigen; antibody; immunoassay; assay; core protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21 DVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGFRQPIPKARQP 71
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Han J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kolberg JA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26.7%; Score 51; DB 2; llarity 100.0%; Pred. No. 8e-39; Conservative 0; Mismatches 0
                                                                                                                                                                  Hepatitis C virus Jl isolate core protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Irvine BD,
  Ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 6; Fig 18; 44pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INST OF HEALTH JAPAN
97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      89US-00408045.
89US-00456142.
91US-00637380.
93US-00101280.
94US-00201066.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   94US-00334255
  AAW30597 standard; protein;
                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Miyamura T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1999-105191/09.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Weiner AJ, Miyam.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (NAHE-) NAT INST OF
(CHIR ) CHIRON CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                          Hepatitis C virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21
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Gaps

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Best Local

Matches

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Hepatitis C virus Jl domain consensus amino acid sequence.
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01-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      core;
                                                                                                                                                                                                                                                                                                                                                                         Saito I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAM50828;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Peptide
                                               NANBH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HCV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Key
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence is encoded by the consensus sequence of the untranslated and core domains of a new hepatitis C virus (HCV), Jl. The Jl and J7 (also a new HCV isolate) isolates comprise sequences which are distinct from the prototype HCV isolates, HCV1. The specification cross-reactive with HCV-1. The assays are used for diagnosis of HCV infection and to screen donated blood. The anti-HCV antibodies are also useful therapeutically and prophylactically (passive immunisation); in screening for antiviral agents, for isolation, purification and incomplements of the prototy of non-B, non-B hepatitis virus (e.g. by affinity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Immunoassays for Asiatic strains of hepatitis C virus - for diagnosis of infection and screening blood supplies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  identification of non-A, non-B hepatitis virus (e.g. by affinity chromatography) and to raise anti-idiotypic antibodies (useful for treatment or diagnosis and to determine immunogenic regions of the HCV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                  HCV; J7 isolate; J1 isolate; HCV1; immunoassay; asiatic strain; diagnosis; HCV infection; blood screening; immunisation; antiviral.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21 DVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGRRQPIPKARQP 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26.7%; Score 51; DB 2; Length 97; 100.0%; Pred. No. 8e-39; cive 0; Mismatches 0; Indels
                                                                                                     Protein encoded by HCV J1 untranslated and core domains.
      AAY01624 standard; protein; 97 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Fig 18; 43pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                 (NAHE-) NAT INST OF HEALTH JAPAN. (CHIR ) CHIRON CORP.
                                                                                                                                                                                                                                                                                                                                89US-00456142.
91US-00637380.
93US-00101280.
94US-00201066.
94US-00334255.
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                                                                                                                                                                                                                                                                                    95US-00436965
                                                                       (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Miyamura T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1999-166619/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                   Hepatitis C virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1999-166619/
N-PSDB; AAX26743.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 97 AA;
                                                                       21-JUN-1999
                                                                                                                                                                                                                                                                                  08-MAY-1995;
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04-JAN-1991;
                                                                                                                                                                                                                                                                                                                                                                  02-AUG-1993;
24-FEB-1994;
                                                                                                                                                                                                                                                                                                                                                                                                  03-NOV-1994;
                                                                                                                                                                                                                  US5871903-A
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                                       AAY01624;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Saito I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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Best Loc Matches

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RESULT 5
ADF66080
ID ADF6
XX
AC ADF6
XX
DT 12-F1

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depatitis C virus; HCV; screening; identification; non A non B hepatitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention describes polynucleotides sequences from Hepatitis C virus (HCV) isolates J7 C/E, J1 E, J1 E/NS1, J1 NS3, and J1 NS5 or from deposits BP-2593, BP2594, BP-2595, BP-2637 and BP-2638. The polynucleotide sequences are useful as probes for screening and
                                                                                                                                                                                                                                                                                                                                                                                                                                              Polynucleotide probes useful for screening and identifying carriers of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  identifying carriers of non A non B hepatitis (NANBH). The present sequence is used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            71
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  antigen; immunogen; infection; diagnosis; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26.7%; Score 51; DB 2; Length 97;
100.0%; Pred. No. 8e-39;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAM50828 standard; protein; 120 AA.
                                                                                                                                                                                                                                                                                                         CHIRON CORP.

NAT INST OF HEALTH JAPAN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example; Fig 18; 44pp; English.
                                                                                                                                                                                    89US-00408045.
89US-00456142.
91US-00637380.
93US-00101280.
94US-00231066.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hepatitis C virus core antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28. .42
/label= MDL-3
                                                                                                                                                      95US-00436966
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/label= MDL-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 26.7
Best Local Similarity 100.
Matches 51; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /label= 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                non A non B hepatitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (revised)
                                                                                                                                                                                                                                                                                                                                                             Miyamura T;
                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1999-570774/48.
N-PSDB; ADF66079.
                                                   Hepatitis C virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hepatitis C virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 97 AA;
                                                                                                                                                                                                                                                                                                         (CHIR ) CHIRON
(NAHE-) NAT INS
                                                                                                                                                    08-MAY-1995;
                                                                                                                                                                                                                                      02-AUG-1993;
24-FEB-1994;
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                                                                                   US5959092-A
                                                                                                                                                                                        15-SEP-1989
                                                                                                                     28-SEP-1999
                                                                                                                                                                                                                        04-JAN-1991
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control; proteolytic processing; precursor.

Hepatitis C virus.

EP518313-A2 16-DEC-1992

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The present sequence is that of the core antigen (amino acids 1-120) of
the polyprotein encoded by hepatitis C virus (HCV). A panel of
c verlapping peptides between positions I and 186 of the HCV core region
was synthesised and tested for immunoreactivity with a commercially
available human serum panel. All of the immunoreactivity was concentrated
within the region between amino acids I to 80. The invention provides a
lighly immunoreactive peptides MDL-1 to MDL-6 (see AAMS0816-27) from
c more of immunoreactive peptides MDL-1 to MDL-6 (see AAMS0816-27) from
this region of the core antigen. Each peptide is individually immobilised
to a carrier. The unique combination of HCV core peptides in the MAC
provides higher specificity and sensitivity for detection of human
antibodies specificity to HCV in rapid HCV diagnostic applications. An in
vitro diagnostic method for detecting anti-HCV antibodies in a test
sample and a diagnostic test kit are provided which use the MAC as an
immunoreagent. The HCV MAC may also potentially be used as an immunogen
in vaccine compositions. (Updated on 07-AUG-2003 to correct OS field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                        New hepatitis C virus (HCV) peptides and mosaic antigen composition comprising the peptides, useful as immunoreagents for detecting HCV antibodies infection, or as an immunogen for stimulating production of antibodies against HCV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 59; 59pp; English.
                             48. .65
/label= MDL-5
                                                                                                                                         103. .120
/label= MDL-8
#1. .57
/label= MDL-4
                                                                                   /label= MDL-6
                                                                                                                      /label= MDL-7
                                                                                                                                                                                                                                                                   06-JUL-2001; 2001WO-CA000988
                                                                                                                                                                                                                                                                                                     07-JUL-2000; 2000CA-02311022
                                                                                                    87. .101
                                                                    66. .80
                                                                                                                                                                                                                                                                                                                                                                         Theolis R;
                                                                                                                                                                                                                                                                                                                                        (MEDM-) MEDMIRA INC.
                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2002-179696/23.
                                                                                                                                                                                               WO200204484-A2
                                                                                                                                                                                                                                                                                                                                                                         Chan HKW,
                                                                      Peptide
                                                                                                       Peptide
                                                                                                                                         Peptide
Peptide
                                   Peptide
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                                                         Gaps
                                                                                    21 DVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGRRQPIPKARQP 71
                                                           .,
                           26.7%; Score 51; DB 5; Length 120; 100.0%; Pred. No. 9.5e-39;
                                      100.0%; Prec. ...
                                                           51; Conservative
                           Query Match
Best Local Similarity
Matches 51; Conserv
Sequence 120 AA;
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Sequence 170 AA;

The sequences given in AAR25929-30 and AAR29534-42 represent various clones of the polypeptide core-envelope region of the Hepatitis C Virus (HCV) gene of the invention. These sequences were isolated from the serum of a patient suffering from hepatitis C (HC). The RNA sequences encoding these peptides were converted into CDNA using transcriptase in the primer sequences given in AAQ32540-46. The CDNA sequences isolated represent different alleles of the same region of the HCV gene. The entire HCV protein (see AAR29527) is useful in the core accourate and effective than conventional ones, in the detection of antibodies raised against a vide range of HCVs which have been hardly detected before. The complete compension of an in vitro screening system for a substance capable of specifically supressing or controlling a proteolytic processing of a protein such a substance capable of stall and substance capable of stall and substance of substance capable of stall and substance capable stall substance capable stall and substance capable stall substance capable stall and s

New hepatitis C virus gene and its encoded protein - used for diagnosing and vaccinating against hepatitis C virus infections.

Claim 5; Page 75-76; 305pp; English.

Hayashi N;

Teranishi Y,

Murakami T,

Takahashi K,

Honda Y,

Seki M,

WPI; 1992-417213/51. N-PSDB; AAQ32438.

(MITU) MITSUBISHI KASEI CORP.

91JP-00172794. 91JP-00287008. 91JP-00332329. 92JP-00099957.

92EP-00109812 91JP-00139268

11-JUN-1992; 11-JUN-1991; 12-JUL-1991; 07-OCT-1991; 16-DEC-1991; 20-APR-1992;

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1; core protein; HCV genotyping; antibody; vaccine;
                        Gaps
                                             21 DVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGRRQPIPKARQP 71
                                                                21 DVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGRRQPIPKARQP 71
                        .,
Length 170;
                        0; Indels
 26.7%; Score 51; DB 2; L4 100.0%; Pred. No. 1.3e-38; iive 0; Mismatches 0;
                                                                                                                                                                                                      Hepatitis C virus isolate T10 core protein.
                                                                                                                                  AAR92948 standard; protein; 190 AA
                                                                                                                                                                                 (first entry)
                           51; Conservative
                Local Similarity
                                                                                                                                                                                                                              envelope
                                                                                                                                                                                                                                                                  Hepatitis C virus.
                                                                                                                                                                                                                                                                                         WO9605315-A2.
                                                                                                                                                                                 02-OCT-1996
                                                                                                                                                                                                                                                                                                              22-FEB-1996.
                                                                                                                                                                                                                                          hepatitis.
                                                                                                                                                         AAR92948;
                                                                                                                                                                                                                               HCV; El;
    Query Match
                            Matches
                                                                                                                        AAR92948
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AAR29529 standard; protein; 170 AA

Clone; polypeptide; core-envelope; region; Hepatitis C; Virus; HCV; HC; cDNA; transcriptase; primer; allele; diagnostic; antibody; supress;

HCV core-envelope peptide N3-1.

(first entry)

(revised)

25-MAR-2003 26-APR-1993

RESULT 7
AAR29529
ID AAR2
XX
AAC AAR2
XX
XX
DT 25-M
DT 26-A
XX
DE HCV
XX
XX
XX
XX
CION
XW
CION

AAR29529;

. 0

used ö

of primers

0;

Gaps

Indels

Length 191;

71 ;

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DNA and amino acid sequence of HCV envelope 1 and core proteins - used to determine HCV genotype and as vaccines against HCV infection.
                                                                                                                                                                                                                                                                                                                                                                               Claim 4; Page 191-192; 340pp; English
                                               WPI; 1996-139709/14,
                                                                                                                                                                                                                                                                                                                                              WPI; 1996-139709/14.
                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                      Hepatitis C virus.
                                                                                                                                                                                                                                                                                                                                                     N-PSDB; AAT16623
                                                    N-PSDB; AAT16622
                                                                                                                                       Sequence 190 AA;
                                                                                                                             HCV infection
    15-AUG-1995;
               15-AUG-1994;
                                                                                                                                                                                                                                                                                                     15-AUG-1995;
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                                                                                                                                                                                                                                 02-OCT-1996
                                                                                                                                                             51;
                                                                                                                                                                                                                                                            hepatitis.
                                                                                                                                                                       21
                                                                                                                                                                                                            AAR92949
                                                                                                                                                                                                                       AAR92949
                                                                                                                                                                                                                                                      E1;
                                    Bukh J,
                                                                                                                                                                                                                                                                                                                                     Bukh J,
                                                                                                                                                            Matches
                                                                                                                                                                                                      RESULT 9
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useful for detecting the presence of HCV in a sample, the primers are also useful for HCV genotyping. Proteins encoded by the cDNAs can be used in vaccines for immunishing against HCV infection. The proteins may also be used to detect antibodies against HCV in serum, saliva, lymphocytes or other mononuclear cells. The antibodies may be used in the prevention of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         envelope 1; core protein; HCV genotyping; antibody; vaccine;
                                                                                                                                                                                                                                                 DVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGRRQPIPKARQP
                                                                                                                                                                                                                             21 DVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGRRQPIPKARQP
 isolates. Isolated cDNA sequences are used for the prodn.
                                                                                                                                                                            1.4e-38;
                                                                                                                                                              DB 2;
                                                                                                                                                           26.7%; Score 51; DB 100.0%; Pred. No. 1.4
                                                                                                                                                                                                                                                                                                                                                                                                                                       Hepatitis C virus isolate SA3 core protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 4; Page 219-220; 340pp; English.
                                                                                                                                                                                                                                                                                                                                          AAR92983 standard; protein; 191 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Purcell RH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      95WO-US010398,
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                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Miller RH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1996-139709/14.
                                                                                                                                                                            Local Similarity
tes 51; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hepatitis C virus.
                                                                                                                                Sequence 191 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; AAT16657
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                                                                                                HCV infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO9605315-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hepatitis.
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                                                                                                                                                              Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bukh J,
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Matches
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                                                                                                                                                                                            used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               envelope 1; core protein; HCV genotyping; antibody; vaccine;
                                                                                                                                                                                         DNA and amino acid sequence of HCV envelope 1 and core proteins determine HCV genotype and as vaccines against HCV infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DVKFPGGGUVGGVYLLPRRGPRLGVRATRKTSERSQPRGRRQPIPKARQP 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGRRQPIPKARQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 190;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 51; DB 2; L. Pred. No. 1.4e-38; D. Mismatches 0;
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                                                                                                                                                                                                                                       Claim 4; Page 190-191; 340pp; English
                                                                                                             Purcell RH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      26.,
100.0%; Pr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           표
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    standard; protein; 191
             95WO-US010398,
                                             94US-00290665
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   26.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (USSH ) US SEC DEPT HEALTH
                                                                           (USSH ) US SEC DEPT HEALTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                           Miller RH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Miller RH,
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·;
DNA and amino acid sequence of HCV envelope 1 and core proteins - used to determine HCV genotype and as vaccines against HCV infection.
                                                                                                                                                                         AAR92936-R92987 are HCV core proteins derived from 52 different HCV isolates. Isolated cDNA sequences are used for the prodn. of primers useful for detecting the presence of HCV in a sample, the primers are also useful for HCV genotyping. Proteins encoded by the cDNAs can be used in vaccines for immunising against HCV infection. The proteins may also be used to detect antibodies against HCV in serum, saliva, lymphocytes or other mononuclear cells. The antibodies may be used in the prevention of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21 DVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGRRQPIPKARQP 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21 DVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGRRQPIPKARQP 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26.7%; Score 51; DB 2; Length 191; 100.0%; Pred. No. 1.4e-38; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           51; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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Matches 5
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AAR92936-R92987 are HCV core proteins derived from 52 different HCV

AAR92979 standard; protein; 191 AA.

RESULT 11

(first entry)

02-OCT-1996

AAR92979;

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DNA and amino acid sequence of HCV envelope 1 and core proteins - used to determine HCV genotype and as vaccines against HCV infection.
                                                                                                                                                                                                                                                                                                              isolates. Isolated CDNA sequences are used for the prodn. of primers useful for detecting the presence of HCV in a sample, the primers are also useful for HCV genotyping. Proteins encoded by the CDNAs can be used in vaccines for immunising against HCV infection. The proteins may also be used to detect antibodies against HCV in serum, saliva, lymphocytes or other mononuclear cells. The antibodies may be used in the prevention of
                                                                                                                                                                                                            DNA and amino acid sequence of HCV envelope 1 and core proteins - used determine HCV genotype and as vaccines against HCV infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          envelope 1; core protein; HCV genotyping; antibody; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                AAR92936-R92987 are HCV core proteins derived from 52 different HCV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     71
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1.4e-38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26.7%; Score 51; DB 2;
100.0%; Pred. No. 1.4e-3
ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hepatitis C virus isolate SA5 core protein.
                                                                                                                                                                                                                                                                  Claim 4; Page 196-197; 340pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAR92980 standard; protein; 191 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 4; Page 217; 340pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Purcell RH;
                                                                                                                                Purcell RH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   95WO-US010398.
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                                 95WO-US010398
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                                                                                             (USSH ) US SEC DEPT HEALTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1996-139709/14.
                                                                                                                                Miller RH,
                                                                                                                                                                WPI; 1996-139709/14.
N-PSDB; AAT16629.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 191 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                      infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-AUG-1995;
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                               15-AUG-1995;
                                                                 15-AUG-1994;
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22-FEB-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bukh J,
                                                                                                                                  Bukh J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA and amino acid sequence of HCV envelope 1 and core proteins - used to determine HCV genotype and as vaccines against HCV infection.
                                                                                                                                                                                   envelope 1; core protein; HCV genotyping; antibody; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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Pred. No. 1.4e-38;
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100.0%; Pred. No. 1...
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hepatitis C virus isolate HK4 core protein.
                                                                                                                                                     Hepatitis C virus isolate SA4 core protein.
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Claim 4; Page 216-217; 340pp; English.

Purcell RH;

Miller RH,

Bukh J,

WPI; 1996-139709/14

N-PSDB; AAT16653

(USSH) US SEC DEPT HEALTH.

95WO-US010398 94US-00290665

15-AUG-1995; 15-AUG-1994;

22-FEB-1996

Hepatitis C virus.

hepatitis.

WO9605315-A2

AAR92955 standard; protein; 191 AA.

RESULT 12

02-OCT-1996

Hepatitis C virus.

hepatitis

HCV;

WO9605315-A2

Conservative

51;

Matches

à g

Query Match Best Local Similarity

Sequence 191 AA; HCV infection

. 0

t C

envelope 1; core protein; HCV genotyping; antibody; vaccine;

Hepatitis C virus.

hepatitis E1;

WO9605315-A2

95WO-US010398.

15-AUG-1995; 22-FEB-1996.

Hepatitis C virus isolate SA10 core protein.

(first entry)

02-OCT-1996

AAR92942;

AAR92942 standard; protein; 191 AA.

RESULT 15

AAR92942

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AAR92936-R92987 are HCV core proteins derived from 52 different HCV isolates. Isolated cDNA sequences are used for the prodn. of primers useful for detecting the presence of HCV in a sample, the primers are also useful for HCV genotyping. Proteins encoded by the cDNAs can be used in vaccines for immunising against HCV infection. The proteins may also be used to detect antibodies against HCV in serum, saliva, lymphocytes or other monomuclear cells. The antibodies may be used in the prevention of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA and amino acid sequence of HCV envelope 1 and core proteins - used to determine HCV genotype and as vaccines against HCV infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HCV; E1; envelope 1; core protein; HCV genotyping; antibody; vaccine;
                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                   71
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                                                                                                                                                                                                                                                    DVKFPGGGIVGGVYLLPRRGPRLGVRATRKTSERSQPRGRRQPIPKARQP
                                                                                                                                                                                                                                   DVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGRRQPIPKARQP
                                                                                                                                                                          Length 191;
                                                                                                                                                                                                       0; Indels
                                                                                                                                                                        DB 2; Le
                                                                                                                                                                                                                                                                                                                                                                                                                                      Hepatitis C virus isolate SA7 core protein.
                                                                                                                                                                                                       Mismatches
                                                                                                                                                                        Score 51;
Pred. No.
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                                                                                                                                                           26.7%; Scu-
100.0%; Pre
0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RH;
                                                                                                                                                                                                                                                                                                                                          AAR92981 standard; protein; 191
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Purcell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (USSH ) US SEC DEPT HEALTH.
                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1996-139709/14
                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hepatitis C virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; AAT16655
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                                                                                                                                          Sequence 191 AA;
                                                                                                           HCV infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO9605315-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-AUG-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-AUG-1994;
                                                                                                                                                                                                                                                                                                                                                                                                         02-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22-FEB-1996.
                                                                                                                                                                                                       51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hepatitis.
                                                                                                                                                                                                                                                                                                                                                                          AAR92981;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bukh J,
                                                                                                                                                                                                       Matches
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                                                                                                                                                                                                                                                                                                                                                    DNA and amino acid sequence of HCV envelope 1 and core proteins - used to determine HCV genotype and as vaccines against HCV infection.
                                                                                                                                                                                                                                                                                                                                                                                                               AAR92936-R92987 are HCV core proteins derived from 52 different HCV isolates. Isolated DNA sequences are used for the prodn. of primers useful for detecting the predner of HCV in a sample, the primers are also useful for HCV genotyping. Proteins encoded by the cDNAs can be used in vaccines for immunishing against HCV infection. The proteins may also be used to detect amtibodies against HCV in scrum, saliva, lymphocytes or other mononuclear cells. The antibodies may be used in the prevention of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      71
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 191;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1.4e-38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26.7%; Score 51; DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Preα....
                                                                                                                                                                                                                                                                                                                                                                                        Claim 4; Page 185-186; 340pp; English.
                                                                                                                                                                                                                                                                                        Purcell RH;
                                                                                                                                                                                                                                    94US-00290665
                                                                                                                                                                                                                                                               (USSH ) US SEC DEPT HEALTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                51; Conservative
                                                                                                                                                                                                                                                                                                               WPI; 1996-139709/14.
                                                                                                                                                                                                                                                                                        Miller RH,
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                                                                                                                                                                                                                                                                                                                            N-PSDB; AAT16616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 191 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HCV infection
                                                                                                                                                                                                                                    LS-AUG-1994;
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October 30, 2004, 01:53:46

Search completed: Ob time: 70 secs

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Gaps

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Length 191;

1.4e-38;

Score 51, DB 2; Pred. No. 1.4e-3

26.78;

100.0%; Pred. w...

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51;

Best Loc Matches

21

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Local Similarity

Query Match

DVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGRRQPIPKARQP

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GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
                    Copyright
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OM protein - protein search, using sw model

Run on:

October 30, 2004, 01:49:56 ; Search time 16 Seconds (without alignments) 1148.588 Million cell updates/sec

US-09-084-691B-206 Perfect score:

191 1 MSTLPKPQRKTKRNTNRRPT......CSFSIFLLALLSCLTTPASA 191 Sequence:

OLIGO Gapop 60.0 , Gapext 60.0 Scoring table:

283416 seqs, 96216763 residues Searched:

0 Word size :

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0' Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		Description	denome polyprotein						н			core protein - hep	늉			genome polyprotein				genome polyprotein	genome polyprotein		genome polyprotein		-7	genome polyprotein	genome polyprotein	genome polyprotein	genome polyprotein		
		CI (841362	S41370	S18032	S18031	S19875	PN0677	S18030	S41371	S41365	PQ0804	S41341	S4136B	S41366	S41350	S41351	S41343	841345	841364	S41363	S41346	JN0265	S12707	A44150	JQ1584	GNWVCJ	GNWVC3	GNWVCH	S21336	S41357
		BB	7	N	N	N	~	7	7	0	7	N	7	۲۹	~	7	7	~	7	~	~	~	C)	7	7	N	Н	Н	Н	7	7
		Match Length	114	114	782	782	782	787	3010	112	114	82	112	114	114	115	115	115	115	115	117	118	322	441	513	640	3010	3011	3011	88	108
₩	Query	Match	26.7	26.7	26.7	26.7	26.7	26.7	9	26.2	9	25.7	25.7	25.7	25.7	25.7	25.7	25.7	25.7	25.7	25.7	25.7	25.7	25.7	25.7	25.7	25.7	25.7	25.7	24.6	24.6
		Score	51	51	51	51	51	51	51	20	20	49	49	49	49	49	49	49	49	49	49	49	49	49	49	49	49	49	49	47	47
	Result	No.	1	7	m	4	Ŋ	9	7	œ	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29

	ALIGNMENTS				
genome polyprotein	S41358	01	114	17.8	34
genome polyprotein	S41349	7	115	18.3	32
genome polyprotein	841352	71	125	19.4	3
core protein - hep	POUBUS	7	57	19.9	n (
genome polyprotein	PC1284	71	513	20.9	40
genome polyprotein	S21471	~	369	21.5	41
polyprotein - hepa	S32740	N	189	22.0	42
genome polyprotein	JQ1303	Н	3033	24.6	47
genome polyprotein	GNWVJ8	Н	3033	24.6	47
genome polyprotein	S40770	Н	3011	24.6	47
genome polyprotein	JQ0881	0	874	24.6	47
genome polyprotein	JQ0883	7	874	24.6	47
genome polyprotein	S41354	N	115	24.6	47
genome polyprotein	841353	7	108	24.6	47
denome polyprotein	S41355	7	108	24.6	47
	000140	N	POT.	24.0	7 7

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N;Contains: core protein
C;Species: hepatitis C virus
A;Variety: genotype 4, NI
C;Date: 19-May-1994 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
C;Accession: $41362
R;Van Doorn, L.J.; Kleter, G.E.M.; Brouwer, J.T.
Submitted to the EMBL Data Library, January 1994
A;Poscription: Analysis of hepatitis C virus genotypes 1 to 5 by LiPA.
A;Reference number: $41341
A;Reference number: $41341
A;Reference number: $41341
A;Residues: 1-114 <VAN>
A;Residues: 1-114 <VAN>
A;Residues: 1-114 <VAN>
A;Residues: UNIPROT: 068896; EMBL: Z29465; NID: 9443892; PIDN: CAA82603.1; PID: 94438
A;Experimental source: genotype 4, NI
C;Superfamily: hepatitis C virus genome polyprotein
C;Keywords: capsid protein; core protein; polyprotein
F;1-114/Product: core protein #status predicted <NAT>
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                                                                polyprotein - hepatitis C virus (genotype 4, N1) (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 26.7%; Score 51; DB 2; Length 114; Best Local Similarity 100.0%; Pred. No. 7.5e-43; Matches 51; Conservative 0; Mismatches 0; Indels
RESULT 1
S41362
genome 1
N; Contai
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21 DVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGRRQPIPKARQP 71

Genome polyprotein - hepatitis C virus (genotype 5, N4) (fragment)
NyContains: core protein
C;Specias: hepatitis C virus
A;Variety: genotype 5, N4
C;Date: 19-May-1994 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
C;Accession: \$4130.
R;Van Doorn, L.J.; Kleter, G.E.M.; Brouwer, J.T.
Submitted to the EMBL Data Library, January 1994
A;Description: Analysis of hepatitis C virus genotypes 1 to 5 by LiPA.
A;Reference number: \$41310
A;Reference number: \$41310
A;Recession: \$41370
A;Residues: 1-114 «VANA
A;Residues: 1-114 «VANA
A;Coss-references: UNIPROT: Q68904; EMBL: Z29473; NID: 9443908; PIDN: CAA82611.1; PID: 94439
A;Cross-reference: genotype 5, N4
C;Superfamily: hepatitis C virus genome polyprotein
C;Keywords: capaid protein; core protein; polyprotein
F;1-114/Product: core protein #status predicted «MAT>

26.7%; Score 51; DB 2; Length 114;

Query Match

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A; variety: isolate JK3
C; Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
C; Accession: S19875
R; Honda, M.; Kaneko, S.; Masashi, U.; Kobayashi, K.; Murakami, S.
Bibmitted to the EMBL Data Library, September 1991
A; Description: Sequence analysis of putative structural regions of Hepatitis C Virus isolate number: S18029
                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: UNIPROT:Q08244; GB:L20498; NID:g1381031; PIDN:AAB02608.1; PID:g1381
C;Superfamily: hepatitis C virus genome polyprotein
C;Keywords: glycoprotein; nonstructural protein
F;196,209,234,250,305,325,421,427,452,536,544,560,580,627,649/Binding site: carbohydrat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Variety: isolate JK1
C; Date: 19-May-2000 #sequence_revision 19-May-2000 #text_change 09-Jul-2004
C; Accession: S18030; S33570; A48332; S18029
R; Honda, M.; Kaneko, S.; Masashi, U.; Kobayashi, K.; Murakami, S.
submitted to the EMBL Data Library, September 1991
A; Description: A whole genome of hepatitis C virus cDNA was isolated from a single pati
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (nonstruct
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                                                                                      nonstructural protein 2; NS1/E2 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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N;Contains: capsid protein C; envelope protein M; hepacivirin (EC 3.4.21.98)
protein NS4a; nonstructural protein NS4b; nonstructural protein NS5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26.7%; Score 51; DB 2; Length 782; 100.0%; Pred. No. 3.6e-42;
                                                                (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein 787 - hepatitis C virus (fragment)
                                                             JK3)
                                                                  (isolate
                                                                                      N,Contains: core protein, envelope protein 1; C,Species: hepatitis C virus
                                                                     virus
                                                                     hepatitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               51; Conservative
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                                                                                                                                                                                                                                                                                                                                                            A;Molecule type: genomic RNA
A;Residues: 1-782 <HON>
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A, Molecule type: mRNA
A, Residues: 1-787 < CHO>
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                                                                  genome polyprotein
N;Contains: core pr
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Best Local S
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Best Local
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                                         S19875
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                                                                                                                                                                                                                                                       genome polyprotein - hepatitis C virus (isolate JK4) (fragment)

N;Contains: core protein; envelope protein 1; nonstructural protein 2; NS1/E2 protein

C;Species: hepatitis C virus

C;Species: hepatitis C virus

A;Variety: isolate JK4

C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004

C;Accession: S18032

R;Honda, M.; Kaneko, S.; Masashi, U.; Kobayashi, K.; Murakami, S.

Submitted to the EMBL Data Library, September 1991

A;Deference number: Sequence analysis of putative structural regions of Hepatitis C virus isc

A;Reference number: Sl8029

A;Reference number: Sequence analysis of putative structural regions of Hepatitis C virus isc

A;Residues: 1-782 *HON3

A;Residues: 1-782 *HON3

A;Experimental source: isolate JK4

C;Superfamily: hepatitis C virus genome polyprotein

C;Keywords: capsid protein; core protein; envelope protein; glycoprotein; nonstructural

C;Keywords: capsid protein; core protein; envelope AMMT2,

E;1-1-191/Product: core protein; mstatus predicted *AMMT2,

E;1-101/Product: core protein; mstatus predicted *AMMT2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A Experimental source: isolate JK2
Subperfamily: hepatitis C virus genome polyprotein
C;Superfamily: hepatitis C virus genome polyprotein; glycoprotein; nonstructural
C;Keywords: capsid protein; core protein; envelope protein; glycoprotein; nonstructural
F;1-191/Product: core protein #status predicted <MAT1>
F;392-393/Product: envelope protein; #status predicted <MAT2>
F;384-733/Product: NS1/E2 protein #status predicted <MAT3>
F;734-782/Product: nonstructural protein 2 (fragment) #status predicted <MAT4>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            genome polyprotein - hepatitis C virus (isolate JK2) (fragment)
N;Contains: core protein; envelope protein 1; nonstructural protein 2; NS1/E2 protein
C;Species: hepatitis C virus
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F;384-733/Product: NS1/E2 protein #status predicted <MAT3>
F;734-782/Product: nonstructural protein 2 (fragment) #status predicted <MAT4>
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C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
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Pred. No. 3.6e-42;
                      ö
7.5e-43;
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A;Residues: 1-782 <HON>
A;Cross-references: UNIPROT:068950; EMBL:X61593
                      Mismatches
Pred. No.
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genome polyprotein - hepatitis C virus (genotype 4, N4) (fragment)
N;Contains: core protein
C;Species: hepatitis C virus
N;Contains: core protein
C;Species: hepatitis C virus
A;Variety: genotype 4, N4
C;Date: 19-May-1994 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
A;Reference number: S41341
A;Reference number: S41341
A;References: Unipror: Q68899; EMBL: Z29468; NID: G443898; PIDN: CAA82606.1; PID: G4438
A;Cross_references: Unipror: Genomic Palence Polyprotein
C;Superimental Source: genomic Palence
C;Superimental source: genome polyprotein
C;Repwords: capsid protein; core protein; polyprotein
F;1-114/Product: core protein #status predicted <MAT>
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Cispecies: hepatitis C virus

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N;Contains: core protein
N;Conteins: core protein
A;Variety: genotype 1, N1
C;Date: 19-May-1994 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26.2%; Score 50; DB 2; Length 114; 100.0%; Pred. No. 7.4e-42; ive 0; Mismatches 0; Indels
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C;Superfamily: hepatitis C virus genome polyprotein
C;Keywords: capsid protein; core protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25.7%; Score 49; DB 100.0%; Pred. No. 5.5 iive 0; Mismatches
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A; Residues: 1-82 <SI2>
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C,Superfamily: hydrolase; nyclopatic cepcia
F,2-115,Product: capsid protein M #status predicted cePm>
F,116-191/Product: major envelope protein B #status predicted cMEE>
F,390-792/Product: nonstructural protein NS1 #status predicted cNS1>
F,730-1006/Product: nonstructural protein NS2 #status predicted cNS2>
F,107-1615/Product: hepacivirin #status predicted cNS3>
F,1230-1237/Region: nucleotide-binding motif A (P-loop)
F,1316-1319/Region: DEXH motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     F;1616-1862/Product: nonstructural protein NS4a #status predicted <N4A>
F;1863-2013/Product: nonstructural protein NS4b #status predicted <NB>
F;2014-3010/Product: nonstructural protein NS5 #status predicted <NS5>
F;204-3010/Product: nonstructural protein NS5 #status predicted <NS5>
F;196,209,234,250,305,417,423,448,532,540,556,576,623,645/Binding site: carbohydrate (Aq
                                                                                                           A;Cross-references: UNIPROT:Q68949; EMBL:X61596; NID:g59478; PIDN:CAA43793.1; PID:g59479
A;Experimental source: isolate JK1 from an individual
                                                                                                                                                               R; Honda, M.; Kaneko, S.; Unoura, M.; Kobayashi, K.; Murakami, S.
Arch. Virol. 129, 163-169, 1933
A;Title: Sequence analysis of putative structural regions of hepatitis C virus isolated
A;Reference number: A48332; MUID:93119270; PMID:8380322
A;Accession: S33570
                                                                                                                                                                                                                                                                                                                                                                                          A;Molecule type: genomic RNA
A;Residues: 1-547, Tr, 549-621, Vv, 623-624, S', 626-652, DL', 655-761, Tr, 763-782 <HOW>
A;Cross-references: EMBL:X61591
A;Cross-references: EMBL:X61591
A;Note: this sequence is inconsistent with the nucleotide translation
A;Note: the authors translated the codon AGG for residue 43 as Pro, TGG for residue 320
as Trp, and TTC for residue 771 as Ser
A;Note: sequence extracted from NCBI backbone (NCBIN:121747, NCBIP:121748)
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NyContains: ore protein
C;Species: hepatitis C virus
A;Variety: genotype 5, N5
C;Date: 19-May-1994 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
C;Accession: 541371
Submitted to the EMBL Data Library, January 1994
A;Description: Analysis of hepatitis C virus genotypes 1 to 5 by LiPA.
A;Reference number: S41371
A;Accession: S41371
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A)Residues: 1-112 <VANN
A)Cross-references: UNIPNCT:068905; EMBL:229474
A)Experimental source: genotype 5, NS
C)Superfamily: hepatitis C virus genome polyprotein
C;Neywords: capaid protein; core protein; polyprotein
F;1-112/Product: core protein #status predicted <NAT>
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100.0%; Pred. No. 7.3e-42;
iive 0; Mismatches 0;
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                         A, Molecule type: genomic RNA
A, Residues: 1-3010 <HON>
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Best Local Similarity
Matches 50; Conserv
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Query Match

Matches

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Matches

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A,Cross-references: UNIPROT:Q68894; EMBL:Z29453; NID:g443868; PIDN:CAA82591.1; PID:g4438
                                                                                                                                                                                                                                                                        N.Contains: core protein
C;Species: heparitis C virus
A;Variety: genotype 1, N8
C;Arciesy: genotype 1, N8
C;Accession: 841350
R;van Doorn, L.J.; Kleter, G.E.M.; Brouwer, J.T.
R;van Doorn, L.J.; Kleter, G.E.M.; Brouwer, J.T.
A;Description: Analysis of hepatitis C virus genotypes 1 to 5 by LiPA.
A;Reference number: 841341
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     Gaps
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C; Species: hepatitis C virus
A; Variety genotype 1.0 N9
C; Date: 19-May-1994 #sequence_revision 26-Jul-1996 #text_change 09-Jul
C; Date: 19-May-1994 #sequence_revision 26-Jul-1996 #text_change 09-Jul
B; Van Docrn, 1.J.; Kleter, G.E.M.; Brouwer, J.T.
submitted to the EMBL Data Library, January 1994
A; Description: Analysis of hepatitis C virus genotypes 1 to 5 by LiPA.
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                                                                                                                                                                                                                                                 genome polyprotein - hepatitis C virus (genotype 1, N8) (fragment)
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21 DVKFPGGGOIVGGYYLLPRGPRLGVRATRKTSERSOPRGRRQPIPKAR
21 DVKFPGGGOIVGGYYLLPRRGPRLGVRATRKTSERSOPRGRRQPIPKAR
                                                           21 DVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGRRQPIPKAR
                                                                                                         21 DVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGRRQPIPKAR
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C:Superfamily: hepatitis C virus genome polyprotein
C:Reywords: capsid protein; core protein; polyprotein
C:Reywords: capsid protein; detatus predicted «MAT»
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A,Readidues: 1-115 <VNN
A,Cross-references: UNIPROT:068885; EMBL:Z29454
A,Experimental source: genotype 1, N9
C,Superfamily: hepatitis C virus genome polyprotein
C,Reywords: capsid protein; core protein; polyprotein
F,1-115/Product: core protein #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ch 25.7%; Score 49; DB 2; L. Similarity 100.0%; Pred. No. 7.3e-41; 49; Conservative 0; Mismatches 0;
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     Mismatches
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     49; Conservative
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A; Residues: 1-115 < VAN>
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C,Species: hepatitis C virus
A;Variety: genotype 4, NS
A;Variety: genotype 4, NS
C;Decies: hepatitis C virus
A;Variety: genotype 4, NS
C;Date: 19-may-1994 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
C;Date: 19-may-1994 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
C;Accession: 641366
R;Van Doorn, L.J.; Kleter, G.E.M.; Brouwer, J.T.
submitted to the EMBL Data Library, January 1994
A;Description: Analysis of hepatitis C virus genotypes 1 to 5 by LiPA,
A;Reference number: 841341
A;Reference number: 841346
A;Reference LYPE: genomic RNA
A;Residues: 1-114 <VAN>
A;Cross_references: UNIPROT: Q68900; EMBL: Z29469; NID: 9443900; PIDN: CRAB2607.1; PID: 94439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Reference number: 541341
A;Accession: 541368
A;Molecule type: genomic RNA
A;Residues: 1-114 <VANS
A;Cross-references: UNIPROT:Q68902; EMBL:Z29471; NID:g443904; PIDN:CAA82609.1; PID:g4439
                                                                            A,Molecule type: genomic RNA
A,Residues: 1-112 <VAN>
A,Cross-references: UNIPROT:Q68875; EMBL:Z29444; NID:g443850; PIDN:CAA82582.1; PID:g4438
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N;Contains: core protein
C;Species: hepatitis C virus
A;Variety: genotype 5, N2
C;Date: 19-May:1994 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
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A; Description: Analysis of hepatitis C virus genotypes 1 to 5 by LiPA.
A; Reference number: S41341
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C;Accession: S41568
R;van Doorn, L.J.; Kleter, G.E.M.; Brouwer, J.T.
submitted to the EMBL Data Library, January 1994
A;Description: Analysis of hepatitis C virus genotypes 1 to 5 by LiPA.
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C; Superfamily: hepatitis C virus genome polyprotein
C; Keywords: capsid protein; core protein; polyprotein
F;1-112/Product: core protein #status predicted <MAT>
                                                                                                                                                                                                                                                                                                     25.7%; Score 49; DB 2; Le 100.0%; Pred. No. 7.1e-41; tive 0; Mismatches 0;
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C.Superfamily: hepatitis C virus genome polyprotein
C.Keywords: capaid protein; core protein; polyprotein
F.1-114/Product: core protein #status predicted AMA1
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C;Superfamily: hepatitis C virus genome polyprotein
C;Keywords: capsid protein; core protein; polyprotein
F;1-114/Product: core protein #status predicted <MAT>
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Pred. No. 7.2e-41;
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100.0%; Pred. No. ...
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Best Local Similarity
Matches 49; Conserv
                                                        Accession: S41341
                                                      A; Molecule type:
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Result No.

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Sequence:

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61 RRQPIPKARQPQGRHWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPHWGPNDPRRRSRNLG 120
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MEDLINE-93376778; PubMed-8396266;

MEDLINE-93376778; PubMed-8396266;

MEDLINE-93376778; PubMed-8396266;

MEDLINE-93376778; PubMed-8396266;

MEDLINE-93376778; PubMed-8396266;

MEDLINE-931676; PubMed-8396266;

MEDLINE-9316 of the putative El gene of isolates collected worldwide.";

MEDLINE-9416; MEDLINE-9516, MEDLINE-9616, PubMed-8766, GO:0005198; P:structural molecule activity; IEA.

MEDLINE-PAC: IRR002522; HCV capsid.

MICEPPO: IRR002522; HCV capsid.

MEDLINE-PAC: IRR002522; HCV capsid.

MEDLINE-PAC: MEDLINE-9616, MEDLINE-
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MEDLINE=92279243; PubMed=1317578;
Bukh J., Purcell R.H., Miller R.H.;
Sequence analysis of the 5' noncoding region of hepatitis C virus.";
Proc. Natl. Acad. Sci. U.S.A. 89:4942-4946(1992).
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Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
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Proc. Natl. Acad. Sci. U.S.A. 91:8239-8243(1994)
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Q81264
Q97980
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Q91KG2
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Q91KG3
Q91KG9
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Q91KH0
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Les 191; Conservative
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    (TrEMBLrel.
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Polyprotein (Fragment)
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Q81270 hepatitis c
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1640.247 Million cell updates/sec
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                     GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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### genetic groups.";

### genetic groups.";

### J. Gen. Virol. 76:2329-2335(1995).

### BMBL, D37845; BAA07091.1;

### BMBL, D37845; BAA07091.1;

### BMBL, D37845; BAA07091.1;

### GO; GO:0016021; C:integral to membrane; IEA.

### GO; GO:0019028; C:viral capsid; IEA.

### GO; GO:0019021; C:viral envelope; IEA.

### BC GO; GO:0019031; HCV_core.

### BF Fam; PRO1542; HCV_core:

### BF Fam; PRO1542; HCV_core
Chainuvati T., Iizuka H., Tsuda F., Miyakawa Y., Mayumi M.; "Hepatitis C virus variants from Thailand classifiable into five novel genotypes in the sixth (6b), seventh (7c,7d) and ninth (9b,\ 9c) major
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    136 YIPVVGAPLGGVAAALAHGVRAIEDGINYATGNLPGCSFSIFLLALLSCLTTPASA 191
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NON_TER 414 414 414
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Hepacivirus.
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BEDLINE=96005057; PubMed=7561773;
A Tokita H., Okamoto H., Luengrojanakul P., Vareesangthip K.,
Tokita H., Okamoto H., Luengrojanakul P., Vareesangthip K.,
A Chainuvati T., Izuka H., Tsuda F., Miyakawa Y., Mayumi M.;
Hepatitis C virus variants from Thailand classifiable into five
T genetic groups.
T genetic groups.
T genetic groups.

R GO, GO:0016021; C:integral to membrane; IEA.
R GO, GO:0016021; C:integral to membrane; IEA.
R GO, GO:0019031; C:integral to membrane; IEA.
R GO, GO:0019031; C:viral capsid, IEA.
R GO, GO:0019031; C:viral envelope; IEA.
R GO, GO:0019031; C:viral envelope; IEA.
R GO, GO:0019031; HCV_core.
R InterPro; IPR002521; HCV_core.
R InterPro; IPR002521; HCV_core.
R InterPro; IPR002531; HCV_core.
R InterPro; IPR002531; HCV_core.
R InterPro; IPR002531; HCV_vore.
R Pfam; PF01543; HCV_core;
R Pfam; PF01543; HCV_core;
R Pfam; PF01543; HCV_core;
R Pfam; PF01559; HCV_core.
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Pred. No. 2.5e-105;
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100.0%; Pred. No. ...
0; Mismatches
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                                                                                                                              RRQPIPKARQPQGRHWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPHWGPNDPRRRSRNLG 120
                                                                                KVIDTLITCGFADLMGYIPVVGAPLGGVAAALAHGVRAIEDGINYATGNLFGCSFSIFLLA 180
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MEDITINE=97052554; PubMed=8897188;
MEDITINE=97052554; PubMed=8897188;
MEDITINE=97052554; PubMed=8897188;
MILLONE B., Delage G., Murphy D.G.;
"Identification of numerous hepatitis C virus genotypes in Montreal,"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE=96005057; PubMed=7561773;
Tokita H., Okamoto H., Luengrojanakul P., Vareesangthip K.,
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J. Clin. Microbiol. 34:2815-2818(1996).

R EMBL, 1033435; AAB400301.;

R GO, GO:0019028; C:viral capsid; IEA.

R GO, GO:005198; F:structural molecule activity; IEA.

R GO, GO:0052198; F:structural molecule activity; IEA.

R InterPro; IPR002521; HCV capsid.

R InterPro; IPR002521; HCV capsid.

R Ffam; PF01543; HCV_capsid; 1.

PF Fam; PF01542; HCV_core; 1.

FT NON TER 191 1.1.

FT NON TER 191 1.0.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    191 AA; 20789 MW; F292AB64B56DE30A CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q68411;
01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-UNV-2003 (TrEMBLrel. 24, Last annotation update)
Core protein (Freqment).
Hepatitis C virus type 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Core, env and part of E2/NS1 (Fragment).
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                                                                                                                                                                                                                                                                             181 LLSCLTTPASA 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (TrEMBLrel.
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01-JUN-2003 (TrEMBLrel.
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NCBI_TaxID=42182;
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Length 414; Indels ö

Gaps

RESULT 5 Q75Q30

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21 DVKFPGGGQIVGGVYLLPRKGPRLGVRATRKTSERSQPRGRRQPIFKARQPGGRHWAQPG 80
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Hirano M., Tran H.T., Abe K.;
Hirano M., Tran H.T., Abe K.;
"Genotypic distribution of hepatitis C virus (HCV) in Ho Chi Minh
City, Vietnam: New genotyping systems for identification of Vietnamese
HCV isolates.";
                                                                                               21 DVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGRRQPIPKARQPQGRHWAQPG
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                                                                                                                                                                                                                                                                                                                                                                                                                                Viruses; SERNA positive-strand viruses, no DNA stage; Flaviviridae; Hepacivirus; Hepatitis C virus type 6.
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Hepacivirus; Hepatitis C virus; Hepatitis C virus type 6.
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                     DB 2; Length 117; 4.6e-87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              50.8%; Score 97; DB 2; Length 117; 100.0%; Pred. No. 4.6e-87; ive 0; Mismatches 0; Indels
                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  [1] SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
Hirano M., Tran H.T., Abe K.;
Submitted (PEB-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AB162864; BAD11958.1; -..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AB162864; BAD11958.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        117 AA; 13407 MW; 3EAE29D8CAE789F6 CRC64;
                                                                                                                                                                                                                                                                                                                           075033;
05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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Last annotation update)
                                                                                                                                                                        81 YPWPLYGNEGCGWAGWLLSPRGSRPHWGPNDPRRRSR 117
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                   50.8%; Score 97; DB 100.0%; Pred. No. 4.6 tive 0; Mismatches
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Hepatitis C virus type 6a.
                   Query Match
Best Local Similarity 100.(
Matches 97; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hepatitis C virus type 6a.
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nes 97; Conserv
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03-MAR-2004 (
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Polyprotein (
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SEQUENCE
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BAD11958;
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Matches
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                                                                                                                                    DVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGRRQPIPKARQPQGRHWAQPG 80
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Viruses; 88RNA positive-strand viruses, no DNA stage; Flaviviridae;
Hepacivirus; Hepatitis C virus type 6.
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Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Hepacivirus; Hepatitis C virus type 6.
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                                   Query Match 55.5%; Score 106; DB 2; Length 414; Best Local Similarity 100.0%; Pred. No. 1.7e-95; Matches 106; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                          136 YIPVVGAPLGGVAAALAHGVRAIEDGINYATGNLPGCSFSIFLLAL 181
                                                                                                                                                                                      136 YIPVVGAPLGGVAAALAHGVRAIEDGINYATGNLPGCSFSIFLLAL 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
Hirano M., Tran H.T., Abe K.;
Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
EMBL, ABL62667; BAD11961.1;
InterPro; IPR002522; HCV_capsid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.

Hirano M., Tran H.T., Abe K.;

Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.

EMBL, ABIG2866: BAD11960.1;

InterPro; IPR002522; HCV capsid.

Pfam; PF01543; HCV_capsid, 1.
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SEQUENCE 117 AA; 13441 MW; 9EA99F0E118A3F20 CRC64;
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117 AA; 13407 MW; 3EAE29D8CAE789F6 CRC64;
45072 MW; 6C9E1AFE4642241D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
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(TrEMBLrel. 27, Last sequence update)
(TrEMBLrel. 27, Last annotation update)
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100.0%; Pred. No. 4.6e-87;
tive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                   Created)
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(TrEMBLrel. 27, I
(TrEMBLrel. 27, I
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                                                                                                                                                                                                                                                                                                                                                                                                                        Polyprotein (Fragment)
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Best Local Similarity
 414 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=31655;
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NON TER 1
SEQUENCE 11
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Q75Q30;
05-JUL-2004
05-JUL-2004
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NON TER
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05-JUL-2004
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SEQUENCE
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RESULT 6 Q75Q31

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Length 117; 0; Indels

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21 DVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGRRQPIPKARQPGRHWAQPG 80
                                                                                                                                  21 DVKFPGGGGIVGGVYLLPRRGPRLGVRATRKTSERSQPRGRRQPIPKARQPGRHWAQPG 80
                                     9EA99F0E118A3F20 CRC64;
                                                                                                                                                              81 YPWPLYGNEGCGWAGWILSPRGSRPHWGPNDPRRRSR 117
                                                                                                                                                                         81 YPWPLYGNEGCGWAGWLLSPRGSRPHWGPNDPRRRSR 117
                                                                       100.0%; Pred. No. 4.6e-87; ive 0; Mismatches 0;
                                                              Score 97; DB 2;
                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE=95062197; PubMed=7972001;
                                    13441 MW;
EMBL; AB162867; BAD11961.1;
                                                              50.8%;
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                            117
                                     117 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=11103;
               Polyprotein.
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                                      SEQUENCE
                                                                Query Match
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Hirano M., Tran H.T., Abe K.;
"Genotypic distribution of hepatitis C virus (HCV) in Ho Chi Minh
"Genotypic distribution of hepatitis C virus (HCV) in Ho Chi Minh
City, Vietnam: New genotyping systems for identification of Vietnamese
HCV isolates.";
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Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
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                                                      Gaps
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03-MAR-2004 (TrEMBLrel. 27, Last sequence update)
03-MAR-2004 (TrEMBLrel. 27, Last sequence update)
Polyprotein (Fragment).
Heparitis C virus type 6a.
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Hepacivirus; Heparitis C virus; Hepatitis C virus type 6.
NCBI_TaxID=31655;
                                                                                                                                                                                                                                                                             Polyprotein (Fragment).
Hepatiis C virus type 6.
Viruses; sRNA positive strand viruses, no DNA stage; Flaviviridae;
Hepativirus; Hepatitis C virus; Hepatitis C virus type 6.
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                            Length 117;
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                                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AB162866; BAD11960.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NON TER 117 117 SEQÜENCE 117 AA; 13407 MW; 3EAE29D8CAE789F6 CRC64;
     13407 MW; 3EAE29D8CAE789F6 CRC64;
                                                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        81 YPWPLYGNEGCGWAGWLLSPRGSRPHWGPNDPRRRSR 117
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                                                                                                                                             81 YPWPLYGNEGCGWAGWLLSPRGSRPHWGPNDPRRRSR 117
                                                                                                                               81 YPWPLYGNEGCGWAGWLLSPRGSRPHWGPNDPRRRSR 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 97; DB 2; Le
Pred. No. 4.6e-87;
                             50.8%; Score 97; DB 2; Le
100.0%; Pred. No. 4.6e-87;
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100.0%; Pred. No. ...
0; Mismatches
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                                         100.0%; Pred. No. 4.6.
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                   97; Conservative
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                                                                                                                                                                                                                    PRELIMINARY;
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Best Local Similarity
      117 AA;
                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=31655;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Polyprotein.
NON TER
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03-MAR-2004
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Oxamoro H.;

Oxamoro H.;

Oxamoro H.;

Submitted (AUG-1996) to the EMBL/GenBank/DDBJ databases.

EMBL; D8846; P00804.

EMBL; D8846; P00804.

EMBL; D8846; P00804.

EMBL; P00804; P00804.

EMBL; P00804; P00804.

EMBL; P00804; P00804.

EMBL; P008051; C:integral to membrane, IEA.

GO; GO:0019028; C:viral capsid; IEA.

GO; GO:0019028; C:viral envelope, IEA.

GO; GO:005198; F:structural molecule activity; IEA.

InterPro; IPR005251; HCV_capsid.

InterPro; IPR005519; HCV_capsid.

InterPro; IPR01543; HCV_capsid, I.

Pfam; PP01543; HCV_capsid, I.

Pfam; PP01543; HCV_capsid, I.

Pfam; PP01543; HCV_capsid, I.

Pfam; PP01549; HCV_NS1; I.

R Pfam; PP01549; HCV_NS1; I.

R Pfam; PP01549; HCV_NS1; I.

R Pfam; PP01540; HCV_NS1; I.

R Pfam; PP01560; HCV
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                                                                                                                                                                                                                                                                                                    Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
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01-MAY-1997 (TrEMBLrel. 03, Created)
01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                         Core, env and part of E2/NS1 (Fragment).
Hepatitis C virus.
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Best Local Similarity
[2]
SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tokita H., Okamoto H., Luengrojanakul P., Vareesangthip K., Chainuvati T., Iizuka H., Tsuda F., Miyakawa Y., Mayumi M.; "Hepatitis C virus variants from Thailand classifiable into five novel genotypes in the sixth (6b), seventh (7c,7d) and ninth (9b, 9c) major
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF01560; HCV_NS1; 1.

Coat protein; Envelope protein; Glycoprotein; Nonstructural protein;
Polyprotein; Transmembrane.

NON_TER 414 414 414
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Tokita H., Okamoto H., Tsuda F., Song P., Nakata S., Chosa T.,
Iizuka H., Mishiro S., Miyakawa Y., Mayumi M.;
"Hepatitis C virus variants from Vietnam are classifiable into the seventh, eighth, and ninth major genetic groups.";
Proc. Natl. Acad. Sci. U.S.A. 91:11022-11026(1994).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    genetic groups.";
J. Gen. Virol. 76:2329-2335(1995).

EMBL, D37843; BAA070891;
GG, GG.0016021; C.integral to membrane; IEA.

GG, GG.0016021; C.integral to membrane; IEA.

GG, GG.0005198; P. Setructural molecule activity; IEA.

GG, GG.0005198; P. Setructural molecule activity; IEA.

InterPro; IPR002521; HCV capsid.

InterPro; IPR002521; HCV env.

InterPro; IPR002519; HCV env.

InterPro; IPR002531; HCV env.

InterPro; IPR002531; HCV env.

R InterPro; IPR002531; HCV core.

R Pfam; PF01542; HCV core; 1.
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                                                                                                               01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                     414 AA
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                                                                                                                                                                                          Core, env.and part of E2/NS1 (Fragment).
Hepatitis C virus.
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Hepatitis C virus.
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                                                                   PRELIMINARY;
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                                                                                                                                                                                                                                                                                            NCBI_TaxID=11103;
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Q81329;
               RESULT 12
08126
08126
AC 08126
DT 01-NO
DT 01-UU
DT 01-UU
DE Core,
OS Hepat
OC Virus
RR Chain
RR TOKIL
RA TOKIL
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107 WGPNDPRRKSRNLGKVIDTLITCGFADLMGYIPVVGAPLGGVAAALAHGVRAIEDGINYAT 166
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                                                                                                                                                                      TAY, FOOD 19028; C: Littlegral to membrane; IEA.

R GO; GO: 0015028; C: Viral capsid; IEA.

R GO; GO: 0015028; C: Viral capsid; IEA.

R GO; GO: 0015031; C: Viral capsid; IEA.

R GO; GO: 001598; F: Structural molecule activity; IEA.

InterPro; IPR002521; HCV capsid.

R InterPro; IPR002521; HCV core.

InterPro; IPR002531; HCV core.

R InterPro; IPR002531; HCV core.

R Pfam; PF01543; HCV capsid; 1.

R Pfam; PF01543; HCV core; 1.

R Pfam; PF01550; HCV N31.

R Pfam; PF01550; HCV N31; 1.

R Pfam; PF01550; HCV N31; 1.
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MEDLINE=98378034; PubMed=9714232;
Tokita H., Okamoto H., Iizuka H., Kishimoto J., Tsuda F., Miyakawa Y.,
Mayumi M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "The entire nucleotide sequences of three hepatitis C virus isolates in genetic groups 7-9 and comparison with those in the other eight genetic groups.";

Genetic groups.";

Gen. Virol. 79:1847-1857(1998).

EMBL; D84264; BAA32666.1;

PIR; PQ0804; PQ0804.

MSROPS; 229:001;

MEROPS; 239:001;
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GO: GO: 0016021, C:integral to membrane; IEA.

GO: GO: 0019021, C:viral capaid; IEA.

GO: GO: 0019031, C:viral envelope; IEA.

GO: GO: 00005224; F:ATP binding; IEA.

GO: GO: 0000326; F:ATP-dependent helicase activity; IEA.

GO: GO: 0003968; F:RNA-directed RNA polymerase activity; IEA.

GO: GO: 0003368; F:Structural molecule activity; IEA.

GO: GO: 0005369; F:structural molecule activity; IEA.

GO: GO: 0005508; P:proteolysis and peptidolysis; IEA.

GO: GO: 00065508; P:proteolysis and peptidolysis; IEA.
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Okamoto H.;
Submitted (AUG-1996) to the EMBL/GenBank/DDBJ databases.
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01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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                                                                                          EMBL; D88468; BAA13617.1; -. PIR; PQ0804; PQ0804.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      107 WGPNDPRRRSRNLGKVIDTLTCGFADLMGYIPVVGAPLGGVAAALAHGVRAIEDGINYAT 166
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Chainuvati T., Iizuka H., Tsuda F., Miyakawa Y., Mayumi M.;
Chainuvati T., Iizuka H., Tsuda F., Miyakawa Y., Mayumi M.;
"Hepatitis C virus variants from Thailand classifiable into five novel genotypes in the sixth (6b), seventh (7c,7d) and ninth (9b, 9c) major genetic groups."; sixth (6b), seventh (7c,7d) and ninth (9b, 9c) major Groups."; sixth (6b), seventh (7c,7d) and ninth (9b, 9c) major Go, Go:0016021; C:integral to membrane; IEA.
GO, GO:0016021; C:integral to membrane; IEA.
GO, GO:0019031; C:viral capaid; IEA.
GO, GO:0019031; C:viral envelope; IEA.
GO, GO:0005198; F:structural molecule activity; IEA.
InterPro; IPR002522; HCV_capsid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS00190; CYTOCHROWE C; UNKNOWN 1.
Coat protein; Envelope protein; Glycoprotein; Nonstructural protein;
Polyprotein; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3016 AA; 328032 MW; 4E5CFF96258BCE3B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q81271;
01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-UUN-2003 (TrEMBLrel. 24, Last annotation update)
Core, env and part of E2/NS1 (Fragment).
Hepatitis C virus.
GO; GO:0019079; P:viral genome replication; IEA.
GO; GO:0019087; P:viral transformation; IEA.
InterPro; IPR000345; CytC heme BS.
InterPro; IPR000352; CytC heme BS.
InterPro; IPR002522; HCV capsid.
InterPro; IPR002521; HCV core.
InterPro; IPR002521; HCV core.
InterPro; IPR002531; HCV NS1.
InterPro; IPR004549; HCV NS4.
InterPro; IPR004949; HCV NS4.
InterPro; IPR004968; HCV NS5a.
InterPro; IPR004066; HCV NS5a.
InterPro; IPR004069; PEPLIAGRE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      44.5%; Score 85; DB 2; Le 100.0%; Pred. No. 4.1e-74; ative 0; Mismatches 0;
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                                                                                                                                                                      InterPro; IPR000745; HCV_NS4a.
InterPro; IPR001490; HCV_NS4b.
InterPro; IPR001866; HCV_NS5a.
InterPro; IPR00106; HCV_RGRP.
InterPro; IPR004109; Peptidase_S29.
InterPro; IPR009003; Pept_U39_HCV_NS2.
InterPro; IPR002518; Pept_U39_HCV_NS2.
InterPro; IPR007095; RNA_pol_DS_PS.
InterPro; IPR007095; RNA_pol_DS_PS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    [1] __
SEQUENCE FROM N.A.
MEDLINE=96005057; PubMed=7561773;
                                                                                                                                                                                                                                                                                                                                                                                                PPO1539; HCV env.; 1. PPO1539; HCV NS1; 1. PPO1560; HCV NS1; 1. PPO1560; HCV NS2; 1. PPO1006; HCV NS4; 1. PPO1006; HCV NS4b; 1. PPO101506; HCV NS4b; 1. PPO101506; HCV NS4b; 1. PPO101506; HCV NS4b; 1. PPO0998; Viral_RdRP; 1.
                                                                                                                                                                                                                                                                                                                                                                PF01543; HCV capsid;
PF01542; HCV core; 1.
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Best Local Similarity
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NCBI_TaxID=11103;
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Q81271
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InterPro; IPR002519; HCV_env.
InterPro; IPR002511; HCV_env.
InterPro; IPR002531; HCV_env.
InterPro; IPR01454; HCV_capsid; 1.
Pfam; PP01545; HCV_core; 1.
Pfam; PP01559; HCV_env; 1.
Pfam; PF01560; HCV_NS1; 1.
Coat protein; Envelope protein; Glycoprotein; Nonstructural protein; Polyprotein; Transmembrane.
NON TER 414 414
SEQÜENCE 414 AA; 45148 MW; D63EB7CED5B71776 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Gaps
                                                                                                                                                                                                                                                                                                                                                                      Query Match
42.9%; Score 82; DB 2; Length 414;
Best Local Similarity 100.0%; Pred. No. 7.5e-72;
Matches 82; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  136 YIPVVGAPLGGVAAALAHGVRA 157
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Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 228,
Sequence 161,
Sequence 167,
Sequence 168,
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Sequence 206,
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Sequence 174,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1
Sequence 1
Sequence 1
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Sequence 1
Sequence 1
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/cgn2_6/ptodata/1/jaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/jaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/jaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/jaa/PcTUS_COMB.pep:*
/cgn2_6/ptodata/1/jaa/PcTUS_COMB.pep:*
GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-290-665A-206
PCT-US95-10398-206
US-08-635-806C-228
US-08-290-665A-161
US-08-290-665A-167
US-08-290-665A-167
US-08-290-665A-174
US-08-290-665A-174
US-08-290-665A-199
US-08-290-665A-199
US-08-290-665A-199
US-08-290-665A-201
US-08-290-665
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                                                                                                                                                                                                                                                                           478139 seqs, 66318000 residues
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                                                             - protein search, using sw model
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                                                                                             October 30, 2004, 01:57:19
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Gapop 60.0 , Gapext 60.0
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191
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Maximum DB seq length: 200000000
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               Copyright
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Match
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                                                             OM protein
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                                                                                                                                                            Title:
Perfect
                                                                                            Run on:
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No.
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Sequence 202, App	203		189.	194	189.	194	3. AT	N	Segmence 27, April		197.		217.	217.	1 . Ar	ì	Sequence 20, Appl
PCT-US95-10398-202	PCT-US95-10398-203	PCT-US95-10398-205	US-08-635-886C-189	US-08-635-886C-194	US-08-974-690C-189	US-08-974-690C-194	US-09-539-601-3	US-09-539-601-21	US-09-539-601-27	US-09-539-601-33	US-08-290-665A-197	PCT-US95-10398-197	US-08-635-886C-217	US-08-974-690C-217	US-08-905-054B-1	PCT-US92-07813-1	US-07-681-703B-20
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191	191	191	450	450	450	450	3010	3010	3010	3010	191	191	319	319	75	75	06
26.7	26.7	26.7	26.7	26.7	26.7	26.7	26.7	26.7	26.7	26.7	26.2	26.2	26.2	26.2	25.7	25.7	25.7
51	21	21	21	21	21	21	21	51	51	51	20	20	20	20	49	49	49
28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

Length 191;

Score 191; DB 2; Pred. No. 1e-173;

100.0%; 100.0%; 0;

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RRQPIPKARQPQGRHWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPHWGPNDPRRRSRNLG 120
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                                                                                                                                                  GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: LEROUX-ROELS, Geert
APPLICANT: DELEYS, Robert
APPLICANT: WARRIENS, Geert
APPLICANT: WARRIENS, Geert
TITLE OF INVENTION: INMUNDOMINANT HUMAN T CELL EPITOPES OF HEPATITIS C
CURRENT APPLICATION NUMBER: US/08/635,886C
CURRENT PILING DATE: 1996-04-25
PRIOR APPLICATION NUMBER: EP 93402718.6
PRIOR FILING DATE: 1994-10-28
PRIOR FILING DATE: 1993-11-04
NUMBER OF SEQ ID NOS: 286
SOFTWARE: PATCHIN VERSION 3.1
SEQ ID NO 2.28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 RRQPIPKARQPQGRHWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPHWGPNDPRRRSRNLG
                                                                                                                                                                                                      KVIDTLICGFADLMGYIPVVGAPLGGVAAALAHGVRAIEDGINYATGNLPGCSFSIFLLA
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                                                 1 MSTLPKPQRKTKRNTNRRPTDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRG
                                                                             1 MSTLPKPQRKTKRNTNRRPTDVKFPGGGIVGGVYLLPRRGPRLGVRATRKTSERSQPRG
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                 Indels
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100.0%; Pred. No. 1e-173; ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 228, Application US/08635886C; Patent No. 6555114
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Best Local Similarity 100.
Matches 191; Conservative
                     191; Conservative
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Best Local Similarity
Matches 191; Conserv
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                                                                                                                                                                                                KVIDTLTCGFADLMGYIPVVGAPLGGVAAALAHGVRAIEDGINYATGNLPGCSFSIFLLA 180
                                                                               1 MSTLPKPORKTKRNTNRRPTDVKRPGGGOIVGGVYLLPRRGPRLGVRATRKTSERSOPRG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R.H.
NUCLEOTIDE AND DEDUCED
NUCLEOTE SEQUENCES OF THE ENVELOPE 1 AND
CORE GENES OF ISOLATES OF HEPAITIES C VIRUS
AND THE USB OF REAGENTS DERIVED FROM THESE
SEQUENCES IN DIAGNOSTIC METHODS AND VACCINES
263
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         Indels
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         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 191;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/10398
FILING DATE: 15-AUG-1995
CLASSIFICATION: 15-AUG-1995
CLASSIFICATION: BARA: 08/086,428
FILING DATE: 29 JUNE 1993
FILING DATE: 29 JUNE 1993
FRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/290/665
FILING DATE: 15-AUGUST 1994
ATTORNEY, AGENT INFORMATION:
NAME: RIGHARD W. BORK
REGISTRATION NUMBER: 36,459
                                                                                                                                                                                                                                                                                                                                                                                                                                                  MILLER, R.H. AND
                                                                                                                                                                                                                                                                                                                                                                            SEULT 2
2T-US95-10398-206
Sequence 206, Application PC/TUS9510398
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MORGAN & FINNEGAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: homosapiens
INDIVIDUAL ISOLATE: HK2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 345 PARK AVENUE CITY: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEX: 421792
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: BUCH, J., MIL.
APPLICANT: PURCELL, R.H.
TITLE OF INVENTION: NUCL.
TITLE OF INVENTION: CORE
TITLE OF INVENTION: CORE
TITLE OF INVENTION: SEQUINGES: 263
CORRESPONDENCE ADRESS:
                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                               181 LLSCLTTPASA 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NEW YORK
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                                                                                                                            61
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             Matches
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COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/290,665A
FILING DATE: 15-AUG-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2026-4116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 167, Application US/08290665A Patent No. 5882852
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FINNEGAN
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NAME: RICHARD W. BORK
REGISTRATION NUMBER: 36,459
REFRENCE/DOCKET NUMBER: 202
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 751-6849
                                                                                                TELEX: 421792
INFORMATION FOR SEQ ID NO: 161:
SEQUENCE CHARACTERISTICS:
LENGTH: 191 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
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TE
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                     (212) 758-4800
(212) 751-6849
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TITLE OF INVENTION: AMINO A
TITLE OF INVENTION: CORE GE
TITLE OF INVENTION: CORE GE
TITLE OF INVENTION: SEQUENC
NUMBER OF SEQUENCES: 263
CORRESPONDENCE ADDRESSE:
ADDRESSEE: ADDRESSE:
STREET: 345 PARK AVENUE
                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: homosapiens
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INDIVIDUAL ISOLATE: SA10
US-08-290-665A-161
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INDIVIDUAL ISOLATE: T10
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                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: unknown ORIGINAL SOURCE:
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TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: NEW YORK STATE: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-290-665A-167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10154
                          TELEPHONE:
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                                                             TELEFAX:
TELEX: 42
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ZIP: 101
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                                   TITLE OF INVENTION: IMMUNODOMINANT HUMAN T CELL EPITOPES OF HEPATITIS C TITLE OF INVENTION: UNRUS PILE REPERENCE: 2551-94 CURRENT APPLICATION NUMBER: US/08/974,690C CURRENT APPLICATION NUMBER: US/08/974,690C CURRENT FILING DATE: 1997-11-19 PRIOR FILING DATE: 1997-11-19 PRIOR FILING DATE: 1993-11-04 PRIOR FILING DATE: 1993-11-04 SEQ ID NOS: 286 SOFTWARE: PATENTIN VERSION 3.1 SEQ ID NO 228 BEQ ID NO 228 BEQ ID NO 228 BEQ ID NO 228 BEQ ID NO 228 BED IN 1993-11-04 CARRENT SEQ ID NO 228 BEQ ID NO 228 BED IN 1993-11-04 CARRENT SEQ ID NO 228 BEQ ID NO 228 BEQ ID NO 228 BEQ ID NO 228 BED IN 1993-11-04 CARRENT SEQ ID NO 228 CARRENT SEQ ID 
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APPLICANT: BURCELL, R.H.
TITLE OF INVENTION: NUCLECTIDE AND DEDUCED
TITLE OF INVENTION: AMINO ACID SEQUENCES OF THE ENVELOPE 1 AND
TITLE OF INVENTION: CORE GENES OF ISOLATES OF HEPATITIS C VIRUS
TITLE OF INVENTION: AND THE USE OF REAGENTS DERIVED FROM THESE
TITLE OF INVENTION: SEQUENCES IN DIAGNOSTIC METHODS AND VACCINES
CORRESPONDENCE ADDRESS:
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100.0%; Pred. No. 1.6e-173;
rative 0; Mismatches 0; Indels
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15-AUG-1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
COMPUTER: ISM PC COMPATIBLE
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/290,66
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REGISTRATION NUMBER: 36,459
REFERENCE/DOCKET NUMBER: 20
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TYPE: PRT
; ORGANISM: hepatitis C virus
US-08-974-690C-228
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.
Matches 191; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LLSCLTTPASA 191
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COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY I
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-290-665A-161
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APPLICANT:
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Gaps
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APPLICANT: PURCELL, R.H.
TITLE OF INVENTION: AMINO ACID SEQUENCES OF THE ENVELOPE 1 AND
TITLE OF INVENTION: AMINO ACID SEQUENCES OF THE ENVELOPE 1 AND
TITLE OF INVENTION: AND THE USE OF REAGENTS DERIVED FROM THESE
TITLE OF INVENTION: SEQUENCES IN DIAGNOSTIC METHODS AND VACCINES
                                                                ;
                                                                                                      21 DVKFPGGGQIVGGVYLLPRRGPRLGVRATRKISERSQPRGRRQPIPKARQP 71
                                                                                                                                            21 DVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGRRQPIPKARQP
                Score 51; DB 2; Length 191;
Pred. No. 1.1e-40;
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Pred. No. 1.1e-40;
                                                              Indels
26.7%; Stor. 100.0%; Pred. No. ... 0; Mismatches
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100.0%;
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Best Local Similarity
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AMINO ACID SEQUENCES OF THE ENVELOPE 1 AND CORE GENES OF ISOLATES OF HEPATITIS C VIRUS AND THE USE OF REAGENTS DERIVED FROM THESE SEQUENCES IN DIAGNOSTIC METHODS AND VACCINES
                AND THE USE OF REAGENTS DERIVED FROM THESE SEQUENCES IN DIAGNOSTIC METHODS AND VACCINES
CORE GENES OF ISOLATES OF HEPATITIS C VIRUS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 191;
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NUCLEOTIDE AND DEDUCED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MILLER, R.H. AND
                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/290,665A
FILING DATE: 15-AUG-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 174, Application US/08290665A Patent No. 5882852 GENERAL INFORMATION:
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MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: RICHARD W. BORK
REGISTRATION NUMBER: 36,459
REFERENCE/DOCKET NUMBER: 2026
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MORGAN & FINNEGAN
                                                                                                                   MORGAN & FINNEGAN
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INFORMATION FOR SEQ ID NO: 172:
SEQUENCE CHARACTERISTICS:
LENGTH: 191 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
                                                                                                                                                                                                                            ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 345 PARK AVENUE CITY: NEW YORK STATE: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: homosapiens INDIVIDUAL ISOLATE: HK3
                                                                                                                                        : 345 PARK AVENUE
NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN &
                                                                       NUMBER OF SEQUENCES: 20 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: PURCELL, R
TITLE OF INVENTION: NI
TITLE OF INVENTION: C,
TITLE OF INVENTION: C,
TITLE OF INVENTION: A)
TITLE OF INVENTION: A)
WUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
    TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                    STATE: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     USA
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US-08-290-665A-174
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                                                                                                                   ADDRESSEE:
STREET: 34
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                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP:
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           Gaps
                                                                                                                                                                                                                                                                                                                           NUCLEOTIDE AND DEDUCED ANTINO ACID SEQUENCES OF THE ENVELOPE 1 AND CORE GENES OF ISOLATES OF HEPATITIS C VIRUS AND THE USE OF REAGENTS DERIVED FROM THESE SEQUENCES IN DIAGNOSTIC METHODS AND VACCINES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 172, Application US/08290665A
Sequence 172, Application US/08290665A
Patent No. 5882852
GENERAL INFORMATION:
APPLICANT: BUKH, J., MILLER, R.H. AND
APPLICANT: PURCELL, R.H.
APPLICANT: PURCELL, R.H.
APPLICANT: PURCELL, R.H.
ATILE OF INVENTION: AMINO ACID SEQUENCES OF THE ENVELOPE 1 AND
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                                                       21 DVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGRRQPIPKARQP 71
                                                                                            21 DVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSBRSQPRGRRQPIPKARQP 71
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 26.7%; Score 51; DB 2; Length 191
Best Local Similarity 100.0%; Pred. No. 1.1e-40;
Matches 51; Conservative 0; Mismatches 0; Indels
             Indels
             ..
                0; Mismatches
                                                                                                                                                                                                                                                                                   MILLER, R.H. AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/290,665A
FILING DATE: 15-AUG-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2026-4116
                                                                                                                                                                                                                  Sequence 168, Application US/08290665A Patent No. 5882852 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: RICHARD W. BORK
REGISTRATION NUMBER: 36,459
REFERENCE/DOCKET NUMBER: 2026
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEPAX: (212) 751-6849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: MORGAN & FINNEGAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEX: 421792
INFORMATION FOR SEQ ID NO: 168:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FLOPPY DISK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
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amino acid
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                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: NUCL
TITLE OF INVENTION: AMIN
TITLE OF INVENTION: CORE
TITLE OF INVENTION: AND
TITLE OF INVENTION: SEQU
NUMBER OF SEQUENCES: 263
CORRESPONDENCE ADDRESS:
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                  51; Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY I
                                                                                                                                                                                                                                                                                      APPLICANT: BUKH, J., APPLICANT: PURCELL, J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: unknown
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                  Matches
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ORGANISM: homosapiens; individual isolaTE: Z/US-08-290-665A-191
    STRANDEDNESS: unknown
                        TOPOLOGY: unknown ORIGINAL SOURCE:
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NEW YORK
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STATE:
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Best Local
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Patent No. 588285
GENERAL INFORMATION:
APPLICANT: BUKH, J., MILLER, R.H. AND
APPLICANT: BUKH, J., MILLER, R.H.
TITLE OF INVENTION: MUCLECTIDE AND DEDUCED
TITLE OF INVENTION: AMINO ACID SEQUENCES OF THE ENVELOPE 1 AND
TITLE OF INVENTION: CORE GENES OF REAGENTS OF HEPATITIS C VIRUS
TITLE OF INVENTION: SEQUENCES IN DIAGNOSTIC METHODS AND VACCINES
NUMBER OF SEQUENCES: 263
CORRESPONDENCE ADDRESS: 263
ADDRESSEE: MORGAN & FINNEGAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21 DVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGRRQPIPKARQP 71
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/290,665A
FILING DATE: 15-AUG-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/290,665A
FILING DATE: 15-AUG-1994
CLASSIFICATION: 435
                                                                                                                                                    2026-4116
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                                                                              ATTORNEY/AGENT INFORMATION:
NAME: RICHARD W. BORK
REGIESTRATION NUMBER: 36,459
REFERENCE/DOCKET NUMBER: 2026
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEPHONE: (212) 751-6849
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NAME: RICHARD W. BORK
REGISTRATION NUMBER: 36,459
REFRENCE/DOCKET NUMBER: 2026
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
                                                                                                                                                                                                                               TELEX: 421792
INFORMATION FOR SEQ ID NO: 174:
SEQUENCE CHARACTERISTICS:
LENGTH: 191 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
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INFORMATION FOR SEQ ID NO: 191:
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LENGTH: 191 amino acid
TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: MORGAN & FIN
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
                                                                                                                                                                                                                                                                                                                                                          unknown
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TELEX: 42
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                                                                                                                                                                                                                                                                                                                       APPLICANT: BUKH, J., MILLER, R.H. AND
APPLICANT: PURCELL, R.H.
TITLE OF INVENTION: MUCLEOTIDE AND DEDUCED
TITLE OF INVENTION: AMINO ACID SEQUENCES OF THE ENVELOPE 1 AND
TITLE OF INVENTION: AND THE USE OF REAGENTS OF HERATITS C VIRUS
TITLE OF INVENTION: AND THE USE OF REAGENTS DERIVED FROM THESE
TITLE OF INVENTION: SEQUENCES IN DIAGNOSTIC METHODS AND VACCINES
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                                                                                                21 DVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGRRQPIPKARQP 71
                                                                                                                          21 DVKFPGGGGIVGGVYLLPRRGPRLGVRATRKTSERSOPRGRROPIPKAROP 71
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         Length 191;
                                                   0; Indels
26.7%; Score 51; ____.
100.0%; Pred. No. 1.1e-40;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADPLICATION NUMBER: US/08/290,665A
FILING DATE: 15-AUG-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: RICHARD W. BORK
REGISTRATION NUMBER: 36,459
REFERENCE/POCKET NUMBER: 2026-4116
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 756-4800
                                                                                                                                                                                                                                                       ; Sequence 198, Application US/08290665A; Patent No. 5882852; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MORGAN & FINNEGAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: homosapiens INDIVIDUAL ISOLATE: SA4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         263
                            l Similarity 100.
51; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEX: 421792
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
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FILING DATE: 15-AUG-1994
CLASSIFICATION: 435
CTASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: RICHARD W. BORK
REGISTRATION NUMBER: 36,4
                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 191 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
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INDIVIDUAL ISOLATE: SA7
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 191 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: FURCELL, R.H.
TITLE OF INVENTION: AMIN
TITLE OF INVENTION: AMIN
TITLE OF INVENTION: CORE
TITLE OF INVENTION: AND
TITLE OF INVENTION: SEQUENCES, SEGUENCES, 263
NUMBER OF SEGUENCES, 263
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         unknown
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Best Local Similarity
             NEW YORK
                                         USA
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                                                       10154
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                                         COUNTRY:
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AMINO ACID SEQUENCES OF THE ENVELOPE 1 AND
CORE GENES OF ISOLATES OF HEPATITIS C VIRUS
AND THE USE OF REAGENTS DERIVED FROM THESE
SEQUENCES IN DIAGNOSTIC METHODS AND VACCINES
                                                                                                                                          AMINO ACID SEQUENCES OF THE ENVELOPE 1 AND CORE GENES OF ISOLATES OF HEBATITIES C VIRUS MAID THE USE OF REAGENTS DERIVED FROM THESE SEQUENCES IN DIAGNOSTIC METHODS AND VACCINES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 26.7%; Score 51; DB 2; Lv Best Local Similarity 100.0%; Pred. No. 1.1e-40; Matches 51; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/290,665A
FILING DATE: 15-AUG-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 200, Application US/08290665A
Patent No. 5882852
GENERAL INFORMATION:
APPLICANT: BUKH, J., MILLER, R.H. AND
APPLICANT: PURCELL, R.H.
                                     Sequence 199, Application US/08290665A; Patent No. 5882852; GENERAL INFORMATION: APPLICANT: BUKH, J., MILLER, R.H. AND APPLICANT: PURCELL, R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2026-4116
                                                                                                                                               TITLE OF INVENTION: MUCLEOTIDE AN TITLE OF INVENTION: AMINO ACID SI TITLE OF INVENTION: CORE GENES OF TITLE OF INVENTION: SEQUENCES IN NUMBER OF SEQUENCES: 263
CORRESPONDENCE ADDRESS: ADDRESSE: ADDRESSE: MORGAN & FINNEGAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY AGENT INFORMATION:
NAME: RICHARD W. BORK
REGIETRATION UNUMBER: 36,459
REFERENCE/DOCKET NUMBER: 2026-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
TELEX: 421792
INFORMATION FOR SEQ ID NO: 199:
SEQUENCE GHARACTERISTICS:
LENGTH: 191 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               E: MORGAN & FINNEGAN
345 PARK AVENUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
                                                                                                                                                                                                                                                                                                                           STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
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INDIVIDUAL ISOLATE: SA5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                           NEW YORK
: USA
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RESULT 12
US-08-290-665A-199
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STATE: NEW YORK

COMPTREE: USA

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US-08-290-665A-202

| Sequence 202, Application US/08290665A
| Patent No. 58828E2
| GENERAL INFORMATION:
| APPLICANT: BUKH, J., MILLER, R.H. AND
| TITLE OF INVENTION: AMINO ACID SEQUENCES OF THE ENVELOPE 1 AND
| TITLE OF INVENTION: AMINO ACID SEQUENCES OF THE ENVELOPE 1 AND
| TITLE OF INVENTION: AMINO ACID SEQUENCES OF THE ENVELOPE 1 AND
| TITLE OF INVENTION: AMINO THE USE OF REAGGENTS DEFIVED FROM THESE
| TITLE OF INVENTION: SEQUENCES IN DIAGNOSTIC METHODS AND VACCINES
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26.7%; Score 51; DB 2; Length 191;
Best Local Similarity 100.0%; Pred. No. 1.1e-40;
Matches 51; Conservative 0; Mismatches 0; Indels
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COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDERFEGT 5.1
CURRENT APPLICATION DATA:
FLIJING DATE: 15-AUG-1994
CLASSIFICATION: 435
ATTORNEY, AGENT INFORMATION:
NAME: RICHARD W. BORK
REGISTRATION NUMBER: 36,459
REGISTRATION NUMBER: 36,459
REFERENCE/DOCKET NUMBER: 2026-4116
TELECOMMUNICATION:
TELECOMMUNIC
REFERENCE/DOCKET NUMBER: 2026-4116
TELECOMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
                                                                                                                                                      TELEX: 421792
INFORMATION FOR SEQ ID NO: 201:
SEQUENCE CHARACTERISTICS:
LENGTH: 191 amino acids
TYPE: amino acid
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INFORMATION FOR SEQ ID NO: 202:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: homosapiens
INDIVIDUAL ISOLATE: SAI
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CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 191 amino acids
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INDIVIDUAL ISOLATE: SA3
US-08-290-665A-202
                                                                                                                                                                                                                                                                                                                                                                                    unknown
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MEDIUM TYPE: FLOPPY I
                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: unknown ORIGINAL SOURCE:
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        Query Match
        26.7%;
        Score 51;
        DB 2;
        Length 191;

        Best Local Similarity 100.0%;
        Pred. No. 1.1e-40;
        Assatches
        51;
        Conservative 0;
        Mismatches 0;
        Indels 0;
        Gaps 0;

        Qy
        21 DVKFPGGGQIVGGVYLLPRRGPRIGVRATRKTSERSQPRGRRQPIPKARQP 71
        Db
        21 DVKFPGGGQIVGGVYLLPRRGPRIGVRATRKTSERSQPRGRRQPIPKARQP 71

        Db
        21 DVKFPGGGQIVGGVYLLPRRGPRIGVRATRKTSERSQPRGRRQPIPKARQP 71
        Search completed: October 30, 2004, 02:00:42

        Job time: 21 secs
        21 secs
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Sequence 192, App

Sequence 8, Appliance 29, Appl Sequence 77, Appl Sequence 28, Appl Sequence 225, Appl Sequence 1, Appliance 16, Appl Sequence 16, Appl Sequence 16, Appl Sequence 16, Appl Sequence 14, Appl Sequence 14, Appl Sequence 16, Appl Sequence 164, Appl S

Sequence 20, Appl Sequence 2, Appli Sequence 2, Appli Sequence 1, Appli Sequence 1, Appli Sequence 10, Appli Sequence 10, Appli Sequence 58, Appli Sequence 58, Appli Sequence 58, Appli

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Gaps

0;

Result Š. 9

Perfect score:

Title:

Sequence:

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Scoring table:

Word size :

Searched:

Database :

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Sequence 228, Application US/10651165
| Publication No. US20040047877al
| GENERAL INFORMATION:
| APPLICAMT: LEROUX-ROELS, Geert
| APPLICAMT: LEROUX-ROELS, Geert
| APPLICAMT: BLEYS, Robert
| APPLICAMT: MARKTENS, Geert
| TITLE OF INVENTION UNRUS
| TITLE OF INVENTION UNRUSE: US/10/651,165
| TITLE OF INVENTION NUMBER: US/08/974,690C
| RILE REFERENCE: 2551-94
| CURRENT FILING DATE: 1997-11-19
| PRIOR APPLICATION NUMBER: PCT/FE94/03555
| PRIOR APPLICATION NUMBER: PCT/FE94/03555
| PRIOR APPLICATION NUMBER: EP 93402718.6
| PRIOR PILING DATE: 1993-11-04
| NUMBER OF SEQ ID NOS: 286
| SOFTWARE: Patentin Version 3.1
| SEQ ID NO 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 RRQPIPKARQPQGRHWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPHWGPNDPRRRSRNLG 120
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            US-09-756-875-8

US-09-921-397-77

US-09-921-397-77

US-09-921-397-77

US-09-921-38-28

US-10-651-165-225

US-09-36-786-1

US-09-36-786-1

US-09-851-1

US-09-873-224-166

US-09-871-138-66

US-09-851-138-66

US-09-851-138-66
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US-10-719-619-2
US-10-268-562-1
US-10-450-649-7
US-09-306-780-10
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US-10-365-620-58
US-10-365-620-54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ALIGNMENTS
   ; TYPE: PRT
; ORGANISM: hepatitis C virus
US-10-651-165-228
US-10-651-165-228
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Sequence 194, App
Sequence 17, Appli
Sequence 217, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 16, Appli
Sequence 16, Appli
Sequence 16, Appl
Sequence 16, Appl
Sequence 16, Appl
Sequence 16, Appl
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Sequence 189, App
                                                                                                 October 30, 2004, 01:58:21; Search time 49 Seconds (without alignments) 1263.780 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                        1 MSTLPKPQRKTKRNTNRRPT......CSFSIFLLALLSCLTTPASA 191
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| cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
| cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
| cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
| cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
| cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
| cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
| cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
| cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
| cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*
            GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-10-651-165-189
US-10-651-165-194
US-10-467-000-1
US-10-467-000-1
US-09-21-165-217
US-09-21-397-3
US-09-21-397-3
US-09-891-983A-16
US-09-891-983A-16
US-10-173-480-16
US-10-173-480-16
US-10-173-480-16
US-10-173-480-16
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US-10-173-480-16
US-10-173-480-16
US-10-173-10-16
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                                                                                                                                                                                                                                                                      1370721 seqs, 324215800 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                          Published_Applications_AA:
                                                                      - protein search, using sw model
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                                                                                                                                                             US-09-084-691B-206
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Maximum DB seq length: 200000000
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APPLICANT: LEROUX-ROBLS, Geert
APPLICANT: DELEYS, Robert
APPLICANT: DELEYS, Robert
TITLE OF INVENTION: IMMUNODMINANT HUMAN T CELL EPITOPES OF HEPATITIS C
TITLE OF INVENTION: UNBURSE: US/10/651,165
CURRENT APPLICANTON NUMBER: US/10/651,165
CURRENT APPLICANTON NUMBER: US/10/651,165
PRIOR PILING DATE: 1997-11-19
PRIOR PELLING DATE: 1997-11-19
PRIOR PILING DATE: 1997-11-028
PRIOR PELLCATION NUMBER: EPT/EP94/03555
PRIOR PILING DATE: 1993-11-04
NUMBER OF SEQ ID NOS: 286
SOFTWARE: Patentin Version 3.1
SECTION 2.17
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| APPLICANT: Migliaccio, Giovanni
| APPLICANT: Migliaccio, Giovanni
| APPLICANT: Migliaccio, Giovanni
| APPLICANT: Migliaccio, Giovanni
| APPLICANT: Paconesa, Giacomo
| TITLE OF INVENTION: HEPATITIS C VIRUS REPLICONS AND REPLICON
| TITLE OF INVENTION: ENHANCED CELLS
| FILE REPRENCE: ITRO003P
| CURRENT APPLICATION NUMBER: US/10/467,000
| CURRENT FILING DATE: 2003-07-21
| PRIOR APPLICATION NUMBER: PCT/EP02/00526
| PRIOR FILING DATE: 2003-01-16
| PRIOR FILING DATE: 2001-01-23
| NUMBER OF SEQ ID NOS: 13
| SOFTWARE: FastSEQ for Windows Version 4.0
| LENGTH: 3010
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                                                                    Length 450;
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100.0%; Pred. No. 2.5e-37;
tive 0; Mismatches 0;
                                                            26.7%; Score 51; DB 15; I
100.0%; Pred. No. 5.1e-38;
tive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 1, Application US/10467000
; Publication No. US20040067486A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT ORGANISM: hepatitis C virus
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Matches 51; Conservative
                                                                                                                                    Conservative
                                                                    Query Match
Best Local Similarity
Matches 51; Conserv
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US-10-651-165-217
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US-10-651-165-194
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Sequence 194, Application US/10651165

Publication No. US200400477A1

GENERAL INFORMATION:

APPLICANT: LERKOUX-ROBES, Geert

APPLICANT: DELEXOX, Robert

TITLE OF INVENTION: INMUNODOMINANT HUMAN T CELL EPITOPES OF HEPATITIS C

TITLE OF INVENTION: VIRUS

TITLE OF INVENTION: VIRUS

TITLE OF INVENTION: VIRUS

FILE REFERENCE: 2551-94

CURRENT APPLICATION NUMBER: US/00/51,165

CURRENT FILING DATE: 1997-11-19

PRIOR FILING DATE: 1997-11-19

PRIOR FILING DATE: 1997-11-28

PRIOR FILING DATE: 1993-11-04

SEQIENCE FILING DATE: 1993-11-04

NUMBER OF SEQ ID NOS: 286

SEQIENCE PARCENT NOWERE: PARCENT NUMBER: PARCENT NUMBE
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 189, Application US/10651165
; Publication No. US20040047877A1
; Sequence 189, Application No. US20040047877A1
; GENERAL INFORMATION:
; APPLICANT: ELENOX-NOELS, Geert
; APPLICANT: DELEXS, Robert
; TILLE OF INVENTION: IMMUNODOMINANT HUMAN T CELL EPITOPES OF HEPATITIS C
; TILLE OF INVENTION: UNMUNODOMINANT HUMAN T CELL EPITOPES OF HEPATITIS C
; TILLE OF INVENTION: UNMUNER: US/10/651,165
; CURRENT APPLICATION NUMBER: US/08/974,690C
; FILER REPERENCE: 1997-11-19
; PRIOR APPLICATION NUMBER: PCT/8P94/03555
; PRIOR PILLING DATE: 1997-11-19
; PRIOR FILLING DATE: 1997-11-04
; SOFTWARE: PSEQ ID NOS: 286
; SOFTWARE: PATENTING DATE: 1993-11-04
; SSEQ ID NO 189
; LEMOTH: 450
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                                                                                                                                                  61 RRQPIPKARQPQGRHWAQPGYPWPLYGNBGCGWAGWLLSPRGSRPHWGPNDPRRRSRNLG 120
                                                                                                           121 KVIDTLTCGFADLMGYIPVVGAPLGGVAAALAHGVRAIEDGINYATGNLPGCSFSIFLLA 180
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ORGANISM:
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Best Local
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Matches

RESULT 3

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Gaps

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APPLICANT: HOWARD A. FIELDS AND YURY E. KHUDYAKOV
TITLE OF INVENTION: ANTIGENIC EPITOPES AND MOSAIC POLYPEPTIDES OF HEPATITIS C VIRUS
TITLE OF INVENTION: PROTEINS
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APPLICANT: Shah Dinesh O.
APPLICANT: Shah Dinesh O.
APPLICANT: Shah Dinesh O.
APPLICANT: Dawson, George A.
APPLICANT: Dawson, George A.
APPLICANT: Guiterz, Robin A.
APPLICANT: Guiterz, Robin A.
APPLICANT: Desai, Suresh
APPLICANT: Stewart, James D.
TITLE OF INVENTION: Methods For The simultaneous Detection
TITLE OF INVENTION: Methods For The simultaneous Detection
TITLE OF INVENTION: Methods For The simultaneous Detection
TITLE OF INVENTION: Of HCV Antigens And HCV Antibodies
TITLE REPREBUCE: 6821.US.01
CURRENT APPLICATION NUMBER: US/09/891,983A
CURRENT FILING DATE: 2001-06-26
NUMBER OF SEQ ID NOS: 36
SOFTWARE FREEDRE: BetSEQ for Windows Version 4.0
LENGTH: 94
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100.0%; Pred. No. 9.3e-37;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                    25.7%; Score 49; DB 9;
100.0%; Pred. No. 9e-37;
tive 0; Mismatches 0
                                                                                           FILE REFERENCE: 14114.0349U2
CURRENT PELLICYTION NUMBER: UG/09/758,308
CURRENT FILING DATE: 2001.01-10
PRIOR APPLICATION NUMBER: 06/092,339
PRIOR FILING DATE: 1999-07-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 16, Application US/09891983A; Publication No. US20030108858A1; GENERAL INFORMATION:
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                                                                                                                                                                                                                                           PatentIn version 3.0
                                                                                                                                                                                                                                                                                                           TYPE: PRT
CRGANISM: Hepatitis C Virus
US-09-758-308-1
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Best Local Similarity 100.
Matches 49; Conservative
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SOFTWARE: PatentIn v
SEQ ID NO 1
LENGTH: 91
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           GENERAL INFORMATION:
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Matches
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                                                                                                                                                                                                                                                                                                         APPLICANT: BIORAD PASTEUR
TITLE OF INVENTION: Method for simultaneously detecting an antigen of, and an antibod
TITLE OF INVENTION: against, an infectious microorganism
FILE REPERENCE: BET 03P0456
CURRENT APPLICATION NUMBER: US/10/431,587
CURRENT FILING DATE: 2003-05-08
PRIOR APPLICATION NUMBER: FR 0205808
PRIOR APPLICATION NUMBER: FR 0205808
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn version 3.1
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APPLICANT: HYBRIGENICS
TITLE OF INVENTION:
SID nucleic acids and polypeptides selected from
TITLE OF INVENTION: pathogenic strain of the hepatitis C virus and
TITLE OF INVENTION: pathogenic strain of the hepatitis C virus and
TITLE OF INVENTION: applications thereof
FILE REFERENCE: 84809A - JAZ
CURRENT APPLICATION NUMBER: 2010-09-02
PRIOR APPLICATION NUMBER: EP 0040225.7
PRIOR FILING DATE: 2000-08-03
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                                                                            21 DVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGRRQPIPKARQ
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                                   Indels
              Pred. No. 3.1e-37;
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0
100.0%; Pred. ...
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                                                                                                                                                                                                                                   Sequence 1, Application US/10431587 Publication No. US20040072267A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 3, Application US/09921397; Patent No. US20020151484A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Hepatitis C virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; ORGANISM: Hepatitis C virus
US-09-921-397-3
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SEQ ID NO 3
LENGTH: 77
                                   50; Conservative
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Best Local Similarity
Matches 49; Conserv
              Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
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LENGTH: 75
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Sequence 192, Application US/09899046
Publication No. US20030008274A1
GENERAL INFORMATION:
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US-09-878-281-192
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local S
Matches 49
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Best Local
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APPLICANT: Muerhoff, A. Scott
APPLICANT: Muerhoff, A. Scott
APPLICANT: Jarng, Line
APPLICANT: Gutierrez, Robin A.
APPLICANT: Leary, Thomas P.
APPLICANT: Leary, Thomas P.
APPLICANT: Stewart, James L.
TITLE OF INVENTION: METHODS FOR THE SIMULTANEOUS DETECTION
CURRENT FILING DATE: 2004-01-07
PRIOR APPLICATION NUMBER: US/10/173,480
PRIOR PILING DATE: 2001-06-17
PRIOR APPLICATION NUMBER: 09/891,983
PRIOR FILING DATE: 2001-06-26
NUMBER OF SEQ ID NOS: 63
SOFTWARE: FastSEQ for Windows Version 4.0
APPLICANT: Leary, Thomas P.
APPLICANT: Desai, Suresh
APPLICANT: Desai, Suresh
APPLICANT: Desai, Suresh
TITLE OF INVENTION: METHODS FOR THE SIMULTANEOUS DETECTION
TITLE OF INVENTION: OF HCV ANTIGENS AND HCV ANTIBODIES
TITLE OF INVENTION: 082.10S.Pl
CURRENT APPLICATION NUMBER: US/10/173,480
CURRENT FILING DATE: 2002-06-17
PRIOR APPLICATION NUMBER: 09/891,983
PRIOR FILING DATE: 2001-06-26
NUMBER OF SEQ ID NOS: 63
SOFTWARE: FRASESQ for Windows Version 4.0
SEQ ID NO 16
LENGTH: 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21 DVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGRRQPIPKAR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 25.7%; Score 49; DB 14; I
Best Local Similarity 100.0%; Pred. No. 9.3e-37;
Matches 49; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: Variant - HCV-Core Recombinant US-10-173-480-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: Variant - HCV-Core Recombinant
US-10-753-910-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 16, Application US/10753910 Publication No. US20040185436A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Abbott Laboratories APPLICANT: Shah, Dinesh O.
                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           49; Conservative
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Best Local Similarity
Matches 49; Conserv
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US-09-899-046-192
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US-10-753-910-16
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LENGTH: 94
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APPLICANT:
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  New sequences of hepatitis C virus genotypes for diagnosis, prophylaxis and therapy.
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
                                                                                                                                                                     Patentin Release #1.0, Version #1.25 (EPO)
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100.0%; Pred. No. 9.5e-37;
tive 0; Mismatches 0;
                                                                                                                     COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTARE: Patentin Release #1.0, Ver
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/899,046
FILING DATE:
PROM APPLICATION NUMBER: 08/362,455
TITLE OF INVENTION: New sequences of TITLE OF INVENTION: genotypes for di NUMBER OF SEQUENCES: 270
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Publication No. US20030032005A1
GENERAL INFORMATION:
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APPLICATION NUMBER: 08/362,455
                                                                                                                                                                                                                                                                                                                                                                                : 96 amino acids
amino acid
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 Similarity 100.
49; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-899-046-192
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RESULT 14

US 08/259,721

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APPLICATION NUMBER:
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US-09-873-224-192
; Sequence 192, Application US/09873224
; Publication No. US20030064360A1
; GENERAL INFORMATION:
APPLICANT: <UNKNOWN>
; TITLE OF INVENTION: New sequences of hepatitis C virus
TITLE OF SEQUENCES: 270
; NUMBER OF SEQUENCES: 270
; CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: Patentin Selease #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/873,224
FILING DATE: 05-Jun-2001
CLASSIFICATION NUMBER: 08/362,455
FILING DATE: CUNKNOWN>
PRIOR APPLICATION DATA:
ATTORNEY/AGENT INFORMATION:
MAME: Innogenetics sa.
TELEPHONE: 00 32 9 241 07 11
TELEPHONE: 00 32 9 241 07 11
TELEPRAX: 00 32 9 241 07 11
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SEQUENCE 8, APPLICANT IN USCORDANTION:
APPLICANT PIKE, IAN
ITILE OF INVENTION: HERATITIS C VIRUS PEPTIDES
NUMBER 05 ESQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Suite 701-E Columbia Square
STREET: 555 13th Street, N. W.
CITY: Washington
STATE: D. C.
COUNTRY: U. S.
IIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: PatchITIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE:
FILING FILING DATE:
FILING FILING FILING DATE:
FILING FIL
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Best Local Similarity 100.0%; Pred. No. 9.5e-37;
Matches 49; Conservative 0; Mismatches 0;
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MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 192:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 96 amino acids TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Ghent
COUNTRY: Belgium
ZIP: B-9052
COMPUTER READABLE FORM:
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PRIOR APPLICATION DATA:
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